



## SEQUENCE LISTING

<110> YAMADA, AKIYO  
OZEKI, YOSHIHIRO  
SAITO, TAKEO

<120> SCREENING OF GENES TO GIVE TOLERANCE AGAINST  
ENVIRONMENTAL STRESS AND THE APPLICATIONS

<130> 31671-176817

<140> 10/031,331

<141> 2002-01-18

<150> JP P2000-85377

<151> 2000-03-24

<150> JP P1999-235910

<151> 1999-07-19

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<170> PatentIn Ver. 2.1

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Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr Val Leu Pro Phe Lys

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Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu Ser Phe Ser Ser Lys

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Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp Leu Gln Lys Arg Ile
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Gly Val Thr Ala Glu Tyr Ala Ser
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<213> Bruguiera sexangula

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Val Leu Pro Phe Lys Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu
          35              40              45

Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys
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Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser
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Arg Pro Thr Lys Val Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg
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<222> (81)..(1718)

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ggc gaa cgt cag tcc ggc cag gac gtc cgc act caa aat gtg gtg gca 161  
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ctc gac aag atg cta gtg gat gat att ggt gat gta aca att aca aat 257  
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gat ggt gct acg att ctt aag atg tta gaa gta gag cat cct gca gca 305  
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Lys Thr Ser Met Ser Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe	
160 165 170	
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175 180 185	
cgg ggg gaa atc aaa tat cct atc aag agt ata aat att ttg aaa gct	689
Arg Gly Glu Ile Lys Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala	
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His Gly Lys Ser Ala Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu	
205 210 215	
aat act ggt cgt gct gct caa ggg atg cct atg aga gtt gca cct gca	785
Asn Thr Gly Arg Ala Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala	
220 225 230 235	
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Arg Ile Ala Cys Leu Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu	
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Gly Val Gln Val Leu Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg	
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caa aga gaa gct gat atg aca aag gaa cgg att gag aaa ctc ctg aaa	929
Gln Arg Glu Ala Asp Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys	
270 275 280	
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His Asp Ala Leu Cys Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val	
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Val Ala Gly Gly Gly Ala Val Glu Ala Ala Leu Ser Val His Leu Glu	
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Tyr Leu Ala Thr Thr Leu Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu	
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Phe Ala Glu Ser Leu Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala	
445 450 455	
gcc aaa gat gcc act gaa tta gct gca aaa ctc cgg gct tac cac cat	1505
Ala Lys Asp Ala Thr Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His	
460 465 470 475	
aca gca caa aca aag gct gat aag aaa cat tta tca agc atg gga cta	1553
Thr Ala Gln Thr Lys Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu	
480 485 490	
gac ctt tca aag ggg acc atc cga aac aac tta gaa gct gga gtc att	1601
Asp Leu Ser Lys Gly Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile	
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gaa cct gca atg agc aaa ata aag ata att cag ttt gct act gaa gca	1649
Glu Pro Ala Met Ser Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala	
510 515 520	
gcc ata aca att ctt cga att gat gac atg atc aag ctt gtc aag gat	1697
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&lt;212&gt; PRT

&lt;213&gt; Bruguiera sexangula

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Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn Asp Gly Ala Thr Ile
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Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp Gly Thr Thr Ser Val
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Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala Asn Asp Leu Val Arg
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Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly Tyr Arg Leu Ala Met
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          130          135          140

Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala Lys Thr Ser Met Ser
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Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe Ala Asn Leu Val Val
          165          170          175

Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala Arg Gly Glu Ile Lys
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Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala His Gly Lys Ser Ala
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Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu Asn Thr Gly Arg Ala
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Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala Arg Ile Ala Cys Leu
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gag acg gtg tac gat ttg ggg gcg aaa atg ata gag gca ttg ggg aag 144  
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                                   35                                  40                                  45

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aaa att aca aag ctt ggg cgt tca ttt tcg cgg tct agg gat tac gat 240  
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gcc atg gga cca cag gtg aag ttt gtt cag tgc cct gat ggg gag ctg 288  
 Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu  
                                   85                                  90                                  95

cag aag agg aaa gag gtc gtg cat tgt gtc tca ctg cac gag att gat 336  
 Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp  
                                   100                                  105                                  110

gtt atc aat agc aga aca cag ggg ttt ctt gct ctt ttc acc ggg gat 384  
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Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu	
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Asn Arg Ala Leu Glu Asn Glu Met Ala Pro Ile Leu Val Val Ala Thr	
180 185 190	
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195 200 205	
ggg att cca ata gat ctc ctt gat cga cta ctc att atc aca act caa	672
Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln	
210 215 220	
cct tac aca aag gat gaa att cgt aag att ctg gat atc aga tgt cag	720
Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln	
225 230 235 240	
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Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His	
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att ggg gca gaa aca tcc ttg aga tat gcc atc cat ctc att act gct	816
Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala	
260 265 270	
gca gca ttg gca tgc cag aag cga aag gga aag ctt gtg gaa act gag	864
Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu	
275 280 285	
gac att agt cga gct tac aat ctg ttt ctt gat gta aag aga tct aca	912
Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr	
290 295 300	
cag tac cta ata gag tat cag aat cag tac atg ttt aat gag gca ccg	960
Gln Tyr Leu Ile Glu Tyr Gln Asn Gln Tyr Met Phe Asn Glu Ala Pro	
305 310 315 320	
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325 330	
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 Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp  
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 Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu  
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 Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu  
                   165                  170                  175  
 Asn Arg Ala Leu Glu Asn Glu Met Ala Pro Ile Leu Val Val Ala Thr  
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 Asn Arg Gly Ile Thr Thr Ile Arg Gly Thr Asn Tyr Lys Ser Pro His  
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 Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln  
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 Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln  
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 Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His  
                   245                  250                  255  
 Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala  
   260                  265                  270

Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu  
 275 280 285

Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr  
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 His Pro Lys Asn Tyr Gly Pro Gly Ser Arg Ala Cys Arg Val Cys Gly  
 10 15 20 25

aat ccg cac ggg ttg atc agg aag tac gga ctc atg tgc tgc aga cag 149  
 Asn Pro His Gly Leu Ile Arg Lys Tyr Gly Leu Met Cys Cys Arg Gln  
 30 35 40

tgc ttc cgt agc aat gcc aag gaa att ggc ttc att aag tac cgc 194  
 Cys Phe Arg Ser Asn Ala Lys Glu Ile Gly Phe Ile Lys Tyr Arg  
 45 50 55

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ccccctctttc ggatgagctt taggacaatg ttctcttttag tttatgtatt gttgaacttg 314

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 Ile Asn Ile Val Val Ile Gly His Val Asp Ser Gly Lys Ser Thr Thr  
 10 15 20

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 Thr Gly His Leu Ile Tyr Lys Leu Gly Gly Ile Asp Lys Arg Val Ile  
 25 30 35

gag agg ttt gag aag gaa gct gct gag atg aac aag agg tca ttc aag 198  
 Glu Arg Phe Glu Lys Glu Ala Ala Glu Met Asn Lys Arg Ser Phe Lys  
 40 45 50 55

tat gcc tgg gtg ctt gac aag ctg aag gct gag cgt gag cgt ggt atc 246  
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 60 65 70

acc att gat att gcc ttg tgg aag ttc gag aca acc aaa tat tac tgc 294  
 Thr Ile Asp Ile Ala Leu Trp Lys Phe Glu Thr Thr Lys Tyr Tyr Cys  
 75 80 85

acg gtc att gat gct cct gga cat cgt gac ttt att aag aat atg atc 342  
 Thr Val Ile Asp Ala Pro Gly His Arg Asp Phe Ile Lys Asn Met Ile  
 90 95 100

acc ggg act tcc caa gct gac tgt gct gtc ctc atc att gac tct acc 390  
 Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp Ser Thr  
 105 110 115

act ggt ggc ttt gag gct ggt atc tct aaa gat ggt cag acc cgc gag 438  
 Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr Arg Glu  
 120 125 130 135

cat gcc ctg ctt gcc ttc acc ctt ggt gtt aag caa atg att tgc tgc	486
His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile Cys Cys	
140 145 150	
tgc aac aag atg gat gct acc act tcc aag tat tct aag gca aga tat	534
Cys Asn Lys Met Asp Ala Thr Thr Ser Lys Tyr Ser Lys Ala Arg Tyr	
155 160 165	
gat gaa att gtt aag gaa gtg tca tcc tac ttg aag aag gtt ggt tac	582
Asp Glu Ile Val Lys Glu Val Ser Ser Tyr Leu Lys Lys Val Gly Tyr	
170 175 180	
aac cca gag aag att cct ttt gtc ccc ata tct gga ttt gag ggt gac	630
Asn Pro Glu Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu Gly Asp	
185 190 195	
aac atg att gag aga tcc acc aac ctt gac tgg tac aag ggc cca act	678
Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly Pro Thr	
200 205 210 215	
ctt ctt gag gcc ctg gac atg atc cag gag cca aag agg cca tca gat	726
Leu Leu Glu Ala Leu Asp Met Ile Gln Glu Pro Lys Arg Pro Ser Asp	
220 225 230	
aag ccc ctc cgt ctc cca ctt cag gat gtg tac aag att ggt ggt att	774
Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly Gly Ile	
235 240 245	
ggg aca gtc cca gtg ggt cgt gtt gaa act ggt gtc ctg aag cct gga	822
Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu Lys Pro Gly	
250 255 260	
atg gtt gtt act ttt ggt ccc tca gga ctg acc act gaa gtt aag tct	870
Met Val Val Thr Phe Gly Pro Ser Gly Leu Thr Thr Glu Val Lys Ser	
265 270 275	
gtg gag atg cac cat gaa gct ctc caa gag gct ctt ccc gga gac aac	918
Val Glu Met His His Glu Ala Leu Gln Glu Ala Leu Pro Gly Asp Asn	
280 285 290 295	
gtt ggc ttc aat gtt aag aat gtt tcc gtg aag gat ctt aag cgg ggt	966
Val Gly Phe Asn Val Lys Asn Val Ser Val Lys Asp Leu Lys Arg Gly	
300 305 310	
tat gtt gcc tca aac tcc aag gat gat cct gcc aag gag gca tct agc	1014
Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Glu Ala Ser Ser	
315 320 325	
ttc acc tcc caa gtt atc atc atg aac cac cct ggt cag att gga aat	1062
Phe Thr Ser Gln Val Ile Ile Met Asn His Pro Gly Gln Ile Gly Asn	
330 335 340	
ggg tat gcc cct gtt ctg gat tgc cac acc tct cac att gct gtc aag	1110
Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala Val Lys	
345 350 355	

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ttt tct gag atc ctc aca aag att gat agg cga tct ggc aag gag ctt 1158
Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys Glu Leu
360                      365                      370                      375

gaa aag gag ccc aag ttc ttg aag aat ggt gat gct ggg ttc gtg aag 1206
Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Phe Val Lys
                      380                      385                      390

atg att ccg acc aag cct atg gtg gtg gaa act ttc tcc gag tat cct 1254
Met Ile Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu Tyr Pro
                      395                      400                      405

ccg ctt ggt aga ttt gcc gtc agg gac atg cgc cag act gtt gca gtg 1302
Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val Ala Val
                      410                      415                      420

gga gtc atc aag agt gtc gag aaa aag gaa cct tct gga gct aag gtg 1350
Gly Val Ile Lys Ser Val Glu Lys Lys Glu Pro Ser Gly Ala Lys Val
                      425                      430                      435

act aaa tct gct gcc aag aag ggt ggc aaa tgaaccgtgc aagtcagagt 1400
Thr Lys Ser Ala Ala Lys Lys Gly Gly Lys
440                      445

tgatgtagat gaaggctatt ggaagaataa agactgggcc ctggttagcg gtctaattat 1460

tggatgttca gcagttgggt tcgagaacta cagtttcaat tcagcgccat catcacggag 1520

ctgttggtcc cagaattggg ttcttgaccg tcggtggcat tggctgttgg tttgagtgc 1580

ttctttgtgt catgtttaga ctttatcgga tttgctatct cataaagcgg cttgggaatt 1640

ttaaaaaaaaa aaaaaaaaaa aaaa 1664

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<210> 12
<211> 449
<212> PRT
<213> Bruguiera sexangula

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<400> 12
Met Gly Lys Glu Lys Ile His Ile Asn Ile Val Val Ile Gly His Val
  1                      5                      10                      15

Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Leu Gly
          20                      25                      30

Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu
          35                      40                      45

Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
          50                      55                      60

Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe
          65                      70                      75                      80

Glu Thr Thr Lys Tyr Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg
          85                      90                      95

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Asp	Phe	Ile	Lys 100	Asn	Met	Ile	Thr	Gly 105	Thr	Ser	Gln	Ala	Asp 110	Cys	Ala
Val	Leu	Ile 115	Ile	Asp	Ser	Thr	Thr 120	Gly	Gly	Phe	Glu	Ala 125	Gly	Ile	Ser
Lys	Asp	Gly	Gln	Thr	Arg	Glu 135	His	Ala	Leu	Leu	Ala 140	Phe	Thr	Leu	Gly
Val 145	Lys	Gln	Met	Ile	Cys 150	Cys	Cys	Asn	Lys	Met 155	Asp	Ala	Thr	Thr	Ser 160
Lys	Tyr	Ser	Lys	Ala 165	Arg	Tyr	Asp	Glu	Ile 170	Val	Lys	Glu	Val	Ser 175	Ser
Tyr	Leu	Lys	Lys 180	Val	Gly	Tyr	Asn 185	Pro	Glu	Lys	Ile	Pro	Phe 190	Val	Pro
Ile	Ser	Gly 195	Phe	Glu	Gly	Asp	Asn 200	Met	Ile	Glu	Arg	Ser 205	Thr	Asn	Leu
Asp	Trp	Tyr	Lys	Gly	Pro	Thr 215	Leu	Leu	Glu	Ala	Leu 220	Asp	Met	Ile	Gln
Glu 225	Pro	Lys	Arg	Pro	Ser 230	Asp	Lys	Pro	Leu	Arg 235	Leu	Pro	Leu	Gln	Asp 240
Val	Tyr	Lys	Ile 245	Gly	Gly	Ile	Gly	Thr	Val 250	Pro	Val	Gly	Arg	Val 255	Glu
Thr	Gly	Val	Leu 260	Lys	Pro	Gly	Met	Val 265	Val	Thr	Phe	Gly	Pro 270	Ser	Gly
Leu	Thr	Thr 275	Glu	Val	Lys	Ser	Val 280	Glu	Met	His	His	Glu 285	Ala	Leu	Gln
Glu	Ala 290	Leu	Pro	Gly	Asp	Asn 295	Val	Gly	Phe	Asn	Val 300	Lys	Asn	Val	Ser
Val 305	Lys	Asp	Leu	Lys	Arg 310	Gly	Tyr	Val	Ala	Ser 315	Asn	Ser	Lys	Asp	Asp 320
Pro	Ala	Lys	Glu 325	Ala	Ser	Ser	Phe	Thr 330	Ser	Gln	Val	Ile	Ile	Met 335	Asn
His	Pro	Gly	Gln 340	Ile	Gly	Asn	Gly	Tyr 345	Ala	Pro	Val	Leu	Asp 350	Cys	His
Thr	Ser	His 355	Ile	Ala	Val	Lys	Phe 360	Ser	Glu	Ile	Leu 365	Thr	Lys	Ile	Asp
Arg	Arg 370	Ser	Gly	Lys	Glu	Leu 375	Glu	Lys	Glu	Pro	Lys 380	Phe	Leu	Lys	Asn
Gly 385	Asp	Ala	Gly	Phe	Val 390	Lys	Met	Ile	Pro	Thr 395	Lys	Pro	Met	Val	Val 400



Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp  
 405 410 415

Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Glu Lys Lys  
 420 425 430

Glu Pro Ser Gly Ala Lys Val Thr Lys Ser Ala Ala Lys Lys Gly Gly  
 435 440 445

Lys

<210> 13

<211> 770

<212> DNA

<213> Bruguiera sexangula

<220>

<221> CDS

<222> (2)..(769)

<400> 13

c gat gat atg gac gag gcc aca ccc acc ttt gtt tgg ggc acc aat atc 49  
 Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile  
 1 5 10 15

agc gtg cag gat gtc aag gcc gct att cag atg ttt ttg aag cac ttc 97  
 Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe  
 20 25 30

agg gat agt aat cag agt caa agg aac gag att ttt gaa gaa ggg aag 145  
 Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys  
 35 40 45

tac gtg aaa gcg ata cat aag gtt ctt gaa gtt gaa gga gag tcg ctt 193  
 Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu  
 50 55 60

gat gtt gat gct cgt gat gtg ttt gat tat gat tct gat ttg tat gcc 241  
 Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala  
 65 70 75 80

aag atg att cgg tac cca ctt gag gtt ttg gcc att ttc gac att gtt 289  
 Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val  
 85 90 95

ttg atg gat att gtg agt ttg atc aac cct ttg ttt gag aaa cat gta 337  
 Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val  
 100 105 110

caa gtc agg att ttc aat ctt aag acc tcg att aca atg aga aat ctc 385  
 Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu  
 115 120 125

aac cct tct gat atc gaa aag atg gtg tca ttg aag gga atg ata att 433  
 Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile  
 130 135 140

cgg tgt agt tcc ata ata ccg gag atc agg gaa gca gta ttt aga tgc 481  
 Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys  
 145 150 155 160  
  
 ctt gtt tgt ggc tac ttc tct gat ccc atc gtt gtg gat aga gga cgg 529  
 Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg  
 165 170 175  
  
 ata agt gaa cct aaa gca tgc ttg aaa gag gaa tgt ctt act aag aac 577  
 Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn  
 180 185 190  
  
 tcc atg aca cta gtt cac aat cgt tgc agg ttt gct gat aag cag att 625  
 Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile  
 195 200 205  
  
 gtg agg ctc cag gag aca cct gac gag atc cct gaa gga gga aca cca 673  
 Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro  
 210 215 220  
  
 cac acg gtg agc tta ttg atg cat gac aag ctg gta gat gct gga aag 721  
 His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys  
 225 230 235 240  
  
 cca ggt gac agg gtt gag gtc act gga att tat agg gct atg agt gtt a 770  
 Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val  
 245 250 255

&lt;210&gt; 14

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Bruguiera sexangula

&lt;400&gt; 14

Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile  
 1 5 10 15  
  
 Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe  
 20 25 30  
  
 Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys  
 35 40 45  
  
 Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu  
 50 55 60  
  
 Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala  
 65 70 75 80  
  
 Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val  
 85 90 95  
  
 Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val  
 100 105 110  
  
 Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu  
 115 120 125

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Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile
 130                      135                      140

Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys
145                      150                      155                      160

Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg
                      165                      170                      175

Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn
                      180                      185                      190

Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile
                      195                      200                      205

Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro
                      210                      215                      220

His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys
225                      230                      235                      240

Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val
                      245                      250                      255

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<210> 15
<211> 846
<212> DNA
<213> Mesembryanthemum crystallinum

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<220>
<221> CDS
<222> (39)..(530)

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<400> 15
caaattttct ttgctgaatc gaatctacaa aatacctg atg ggt cag gtt ctt gac 56
                      Met Gly Gln Val Leu Asp
                      1                      5

aaa ttt caa cgt aag caa tgg aga caa aag caa atc cag aag ata aca 104
Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys Gln Ile Gln Lys Ile Thr
                      10                      15                      20

gat aag gta ttt gat cgt gtc aaa agt ccg acc gga aat ggc act ctt 152
Asp Lys Val Phe Asp Arg Val Lys Ser Pro Thr Gly Asn Gly Thr Leu
                      25                      30                      35

aca ttt gaa gag ctg tat ata gct acc ctg att gtc tac aat gat ata 200
Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu Ile Val Tyr Asn Asp Ile
                      40                      45                      50

aac aag tat ttg ccg ggg ccg cac ttt gat cct cca tcg aaa gac aaa 248
Asn Lys Tyr Leu Pro Gly Pro His Phe Asp Pro Pro Ser Lys Asp Lys
55                      60                      65                      70

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atc aga gcc ttg atg cag gaa tgc gat atg gat gtc gat gga gaa ctt 296
Ile Arg Ala Leu Met Gln Glu Cys Asp Met Asp Val Asp Gly Glu Leu
              75                      80                      85

aac cgt gag gaa ttt gtg aag ttc atg cag aag gtg aca gcc gat aca 344
Asn Arg Glu Glu Phe Val Lys Phe Met Gln Lys Val Thr Ala Asp Thr
              90                      95                      100

ttc tct acg gtc agc cag gga ctg att atc tct ctg att ctg gcg cca 392
Phe Ser Thr Val Ser Gln Gly Leu Ile Ile Ser Leu Ile Leu Ala Pro
              105                      110                      115

aca gtt gca ttg gcg acg aag agg gca aca gaa ggt gtt cca ggt gtg 440
Thr Val Ala Leu Ala Thr Lys Arg Ala Thr Glu Gly Val Pro Gly Val
              120                      125                      130

ggg aaa gtg gtg caa aag gtg cct act tca att tat gca tcc ctg gtg 488
Gly Lys Val Val Gln Lys Val Pro Thr Ser Ile Tyr Ala Ser Leu Val
              135                      140                      145                      150

acc ctt gtt gtc gtt gca atc caa act gct agc gag gga tgc 530
Thr Leu Val Val Val Ala Ile Gln Thr Ala Ser Glu Gly Cys
              155                      160

tgattagagg ctttagttac ttgttcatga tacagaagga acagtcttgg tcaatttatt 590
tctttttttaa taggacataa ggaagttgta tatctttctt ctttcttcta ccagggttttg 650
ggggaagtgg gaaagaacat acaaagtatt tcaactgcgt attggctgat cctcccatatt 710
attaaaaactt gtcgtgtcta gcatgagcga ttcaatattt gcaatatgca atatttgtaa 770
tgatgtctac attcagtgat tagtgtgatt gtgcagtttg ttgggaaaaa aaaaaaaaaa 830
aaaaaaaaaa aaaaaa 846

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<210> 16
<211> 164
<212> PRT
<213> Mesembryanthemum crystallinum

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<400> 16
Met Gly Gln Val Leu Asp Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys
  1              5              10              15

Gln Ile Gln Lys Ile Thr Asp Lys Val Phe Asp Arg Val Lys Ser Pro
              20              25              30

Thr Gly Asn Gly Thr Leu Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu
              35              40              45

Ile Val Tyr Asn Asp Ile Asn Lys Tyr Leu Pro Gly Pro His Phe Asp
              50              55              60

Pro Pro Ser Lys Asp Lys Ile Arg Ala Leu Met Gln Glu Cys Asp Met
              65              70              75              80

```

Asp Val Asp Gly Glu Leu Asn Arg Glu Glu Phe Val Lys Phe Met Gln  
85 90 95

Lys Val Thr Ala Asp Thr Phe Ser Thr Val Ser Gln Gly Leu Ile Ile  
100 105 110

Ser Leu Ile Leu Ala Pro Thr Val Ala Leu Ala Thr Lys Arg Ala Thr  
115 120 125

Glu Gly Val Pro Gly Val Gly Lys Val Val Gln Lys Val Pro Thr Ser  
130 135 140

Ile Tyr Ala Ser Leu Val Thr Leu Val Val Val Ala Ile Gln Thr Ala  
145 150 155 160

Ser Glu Gly Cys

<210> 17

<211> 872

<212> DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (183)..(569)

<400> 17

aacaaaatgt ctctctcttt ctctttctct ttctctttct ctctcttcgt gggttgattg 60

agtaagctct gtctttttgc tctctgttga atgtactatc ttctgtgaac caaaggccaa 120

agattaacta ttggagattt ctctactcga aatttgttt taggtgttga ccctgttgag 180

ct atg gcg aac aag ccc caa att cca acg aag aat tcg gcc ctc att 227  
Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile  
1 5 10 15

gct att atc gcg gat gag gat act gta act gga ttt ttg ctg gct gga 275  
Ala Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly  
20 25 30

gtt ggt aat gtt gat cta cga aga cag aca aat tac att att gtg gac 323  
Val Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp  
35 40 45

aat aaa aca acg atg aag caa atc gaa gat gca ttc aag gag ttc aca 371  
Asn Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr  
50 55 60

gca aga gag gac att gcg gtt gta cta atc agc caa tat gtt gca aat 419  
Ala Arg Glu Asp Ile Ala Val Leu Ile Ser Gln Tyr Val Ala Asn  
65 70 75

atg ata aga gta ttg gtt gat agc tac aac aaa cca atc ccg gca att 467  
Met Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile  
80 85 90 95

```

ttg gag att cct tca aag gac cat cct tat gat cct aac cat gat tca 515
Leu Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser
      100              105              110

gtc ctt tca agg gtt aaa tac ctg ttc tct tct gaa tcg gca tca agc 563
Val Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser
      115              120              125

aga ttt tagccatatg ctttgtaaag ttccctgctc ctgaatgttt ggtgattatg 619
Arg Phe

agtttaaaact agaaccagtc acattctgac ttggtatttt gaggcactgt ttgttttatg 679

ttcttaaaat aaggagtgtg attacgactc catgaatcgg gatatgactc catgaatcgc 739

atgtattttct ttccatctca ttgaaagag tcgagcagcc atatcattta gtttcttctc 799

cttgcgaaatg agcttggaag aaatgttttg gctataaaaag atttcaactc ttggtacaaa 859

aaaaaaaaaaa aaa 872

```

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<210> 18
<211> 129
<212> PRT
<213> Mesembryanthemum crystallinum

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<400> 18
Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile Ala
  1              5              10              15

Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly Val
      20              25              30

Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp Asn
      35              40              45

Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr Ala
      50              55              60

Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn Met
      65              70              75              80

Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile Leu
      85              90              95

Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser Val
      100              105              110

Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser Arg
      115              120              125

Phe

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<210> 19
<211> 647
<212> DNA

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<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (64)..(426)

<400> 19

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cttggtttttc tctctctctct ctctctctct tctccgcacc ctcaggcagc gaaggtagca 60

aca atg gcg tac gcg atg aag cca acg aag ccc ggg atg gag gaa tcc 108
  Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser
    1             5             10             15

cag gag cag att cac aag atc agg atc act ctt tct tct aag aac gtc 156
  Gln Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val
                20             25             30

aag aac ctt gag aaa gtg tgt gct gat ctt gta cgc ggt gca aag gac 204
  Lys Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp
                35             40             45

aag cgc ctc agg gtt aag gga cca gtg agg atg ccc acc aag gtt ctg 252
  Lys Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu
                50             55             60

aag atc aca aca agg aag tct ccc tgt ggt gaa gga acc aac acc ttt 300
  Lys Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe
    65             70             75

gac aga ttt gag ttg cgt gtt cac aag aga gtc att gac ctc ttc agc 348
  Asp Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser
    80             85             90             95

tcc cca gac gtg gtc aag cag atc acc tcc atc acc att gaa cct ggt 396
  Ser Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly
                100             105             110

gtt gag gtt gag gtt aca ata gct gac tct tagacatgcc tggtgaagtt 446
  Val Glu Val Glu Val Thr Ile Ala Asp Ser
    115             120

gtcgtcgttg tagggctgtt gtagctgtct catatagtgg tgctatctca ctaagaattt 506

tgaagatact aaattgtttg ttgaaagag atgttttctt tagctgtaat gttatgtttt 566

tgaagggtgtt ggaacatgca ttatttgta atgctttatc aatagaactt ccaatttgaa 626

tgcaaaaaaaaa aaaaaaaaaa a 647

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<210> 20

<211> 121

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 20

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Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser Gln
  1             5             10             15

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Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val Lys  
                   20                  25                  30  
 Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp Lys  
                   35                  40                  45  
 Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu Lys  
                   50                  55                  60  
 Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe Asp  
                   65                  70                  75                  80  
 Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser Ser  
                   85                  90                  95  
 Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly Val  
                   100                  105                  110  
 Glu Val Glu Val Thr Ile Ala Asp Ser  
                   115                  120

<210> 21  
 <211> 686  
 <212> DNA  
 <213> Sueada japonica

<220>  
 <221> CDS  
 <222> (62)..(493)

<400> 21  
 acaccattca caaaacacat taataaaaaaa cactacttct ttcttttotta gccacttgaa 60  
 a atg gcc tac tca aag gct gta ctc ctt gcc ctt atc ttt gct gtg act 109  
   Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr  
       1                  5                  10                  15  
 ctt gtc att gcc tct cag gtc tca gct cgt gaa ctt gct gag gag aca 157  
 Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr  
                   20                  25                  30  
 caa tct gtg gag gag tct aag gga tac ggt ggt ggg cac gga ggt cac 205  
 Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His  
                   35                  40                  45  
 tat ggt ggt ggt cac tat ggt ggt gga cac aga cac ggt ggc cat gga 253  
 Tyr Gly Gly Gly His Tyr Gly Gly Gly His Arg His Gly Gly His Gly  
                   50                  55                  60  
 cac tac gca act gag gaa gca gag aac aag aat gaa gcc gta gaa cct 301  
 His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro  
                   65                  70                  75                  80  
 caa ggc ggc tat ggt cac gga cac gga gga ggc tac gga cac ggt ggt 349  
 Gln Gly Gly Tyr Gly His Gly His Gly Gly Tyr Gly His Gly Gly  
                   85                  90                  95



ggc tac gga cac ggt gga ggc tac gga cac gga ggt ggc tac ggg cac 397  
 Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His  
                   100                  105                  110

ggt ggt ggc tac gga cat gga ggt ggt tat gga cac ggt gga cac ggt 445  
 Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly His Gly  
                   115                  120                  125

gga cat ggt ggt cat ggt cac tac gcc aag act acc gag gaa caa aat 493  
 Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn  
                   130                  135                  140

taagttatgg gttactaaaa cttaaattgt acgttgtcaa ataaaatgta ctttatgatt 553

ttacatgagt atgcatgtaa ttcatacataa gcttcaagga ctatcttgta ctctatgtta 613

tatacctata tgaaatggaa gcgtgacttt tattactgta aaaaaaaaaa aaaaaaaaaa 673

aaaaaaaaaa aaa 686

<210> 22

<211> 144

<212> PRT

<213> Sueada japonica

<400> 22

Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr  
       1                  5                  10                  15

Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr  
                   20                  25                  30

Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His  
                   35                  40                  45

Tyr Gly Gly Gly His Tyr Gly Gly Gly His Arg His Gly Gly His Gly  
                   50                  55                  60

His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro  
                   65                  70                  75                  80

Gln Gly Gly Tyr Gly His Gly His Gly Gly Tyr Gly His Gly Gly  
                   85                  90                  95

Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His  
                   100                  105                  110

Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly His Gly  
                   115                  120                  125

Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn  
                   130                  135                  140

<210> 23

<211> 683

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<210> 24
<211> 105
<212> PRT
<213> Salsola komarovii
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&lt;400&gt; 24

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Met Ala Phe Ser Lys Pro Leu Ile Ala Ser Leu Leu Leu Ser Leu Phe
 1              5              10              15

Val Leu Gln Phe Val His Ala Val Glu Pro Ile Ser Ser Ser Asn Gln
              20              25              30

Val Gly Ser Asn Thr Gly Gly Thr Ser Glu Ser Lys Val Asp Cys Gly
              35              40              45

Ala Ala Cys Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys
 50              55              60

Asn Arg Ser Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro
 65              70              75              80

Gly Thr Ser Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr
              85              90              95

Thr His Gly Asn Arg His Lys Cys Pro
              100              105

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&lt;210&gt; 25

&lt;211&gt; 803

&lt;212&gt; DNA

<213> *Salsola komarovii*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (51)..(593)

&lt;400&gt; 25

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cgcagacgct tcagctcttt ctctctcttt ctctctcctc accgtgaaag atg ggg      56
                                   Met Gly
                                   1

ttg tca ttt acc aaa ttg ttt agc cgg ttg ttc gct aag aag gaa atg      104
Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys Glu Met
              5              10              15

cgt atc ctt atg gtc ggt ctc gat gcc gct ggt aaa acc acc att ctc      152
Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile Leu
              20              25              30

tat aaa ctc aag ctg gga gag att gtc acc acc att cct acc att gga      200
Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile Gly
              35              40              45              50

ttt aat gtg gag act gta gaa tac aag aac atc agc ttc act gtg tgg      248
Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val Trp
              55              60              65

gat gtc ggg ggt caa gac aag att cgt cca ttg tgg aga cat tac ttc      296
Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr Phe
              70              75              80

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caa aac acc caa ggt ctc atc ttt gtg gtt gac agt aat gat cgt gac 344  
 Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp Arg Asp  
           85                                  90                                  95

cgt gtc gtt gag gca aga gat gaa ctg cat agg atg tta aat gag gat 392  
 Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn Glu Asp  
       100                                  105                                  110

gaa tta cga gat gca gtg ttg ttg gtg ttt gca aac aag caa gat ctt 440  
 Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln Asp Leu  
 115                                  120                                  125                                  130

ccc aat gca atg aat gct gct gag atc act gat aag ctt ggt ctc cat 488  
 Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly Leu His  
                                   135                                  140                                  145

tct cta cgt caa cgc cat tgg tac ata caa agc aca tgt gcc acc tct 536  
 Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala Thr Ser  
                                   150                                  155                                  160

gga gaa ggg ctt tac gag ggt ctg gac tgg ctc tca aac aat atc gct 584  
 Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn Ile Ala  
       165                                  170                                  175

agc aag gct taaaagtaac agaacgagta aggttagctt tctcagagaa 633  
 Ser Lys Ala  
       180

gaagctggag tataggctga ggactatcgt tactgctagt gttacccttt ttatttttgc 693

catttatatg ttcacatttt tggttcctat cggacaagaa ttattttctg cgtttatgtt 753

gacttggtat aataccatac ttttttagttg aaaaaaaaaa aaaaaaaaaa 803

&lt;210&gt; 26

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Salsola komarovii

&lt;400&gt; 26

Met Gly Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys  
   1                                  5                                  10                                  15

Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr  
                                   20                                  25                                  30

Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr  
                                   35                                  40                                  45

Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr  
       50                                  55                                  60

Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His  
       65                                  70                                  75                                  80

Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp  
                                   85                                  90                                  95

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<210> 27
<211> 680
<212> DNA
<213> Avicennia marina
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<400> 27																
ctaaaagcca	aaggcaagat	aagaaacagg	ttccttttagc	tatcttcctc	gtctcgctgc											60
tgcaaaagtt	ccatccccag	aagatcagga	aaaccctttct	gcagcagcac	tctaataatc											120
ctccaatttt	gattcaagag	aagaaacaaa	ataaacagaa	atg	gct	cgc	tct	ttc								175
				Met	Ala	Arg	Ser	Phe								
				1				5								
tcc	aac	gct	aag	acc	gtc	tct	gct	gtc	att	gcc	aac	gaa	atc	tca	gct	223
Ser	Asn	Ala	Lys	Thr	Val	Ser	Ala	Val	Ile	Ala	Asn	Glu	Ile	Ser	Ala	
				10					15					20		
ctt	gtc	acc	agg	agg	ggt	tat	gct	gct	ctc	gca	cag	ggc	gtt	gtt	tcg	271
Leu	Val	Thr	Arg	Arg	Gly	Tyr	Ala	Ala	Leu	Ala	Gln	Gly	Val	Val	Ser	
			25					30					35			
agc	agc	gcg	aga	agc	ggc	ggc	gct	ccg	aac	gtg	atg	ctg	aag	aaa	gga	319
Ser	Ser	Ala	Arg	Ser	Gly	Gly	Ala	Pro	Asn	Val	Met	Leu	Lys	Lys	Gly	
		40					45					50				
tcc	gaa	gaa	tcc	ggg	aag	aca	gca	tgg	gtg	ccc	gac	ccg	gac	acc	ggc	367
Ser	Glu	Glu	Ser	Gly	Lys	Thr	Ala	Trp	Val	Pro	Asp	Pro	Asp	Thr	Gly	
	55					60				65						
tac	tac	cga	ccg	gga	aac	gag	gac	aag	gcc	gcg	ctg	gac	ccg	gtc	gag	415
Tyr	Tyr	Arg	Pro	Gly	Asn	Glu	Asp	Lys	Ala	Ala	Leu	Asp	Pro	Val	Glu	
70					75				80						85	

ctg cgg gag atg ctc atc aag aac aag ccc agc cga caa tgaatgaacc 464  
 Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser Arg Gln  
                   90                                  95

aagaattgtg ggattctcat taattcctcc cctgttctgg tccatcgtcg gaatctgaac 524  
 ctgttggtcg tctagaaatt cgttcccatg gaaatctatc aaagtctgta ttcttgccat 584  
 ggctcttcct gtcccatata tgtatgtcct caggtgtggc ctgggggtggg ttgatagata 644  
 tataaaatgt ggtgaattta aaaaaaaaaa aaaaaa 680

<210> 28  
 <211> 98  
 <212> PRT  
 <213> Avicennia marina

<400> 28  
 Met Ala Arg Ser Phe Ser Asn Ala Lys Thr Val Ser Ala Val Ile Ala  
   1                  5                  10                  15  
 Asn Glu Ile Ser Ala Leu Val Thr Arg Arg Gly Tyr Ala Ala Leu Ala  
                   20                  25                  30  
 Gln Gly Val Val Ser Ser Ser Ala Arg Ser Gly Gly Ala Pro Asn Val  
                   35                  40                  45  
 Met Leu Lys Lys Gly Ser Glu Glu Ser Gly Lys Thr Ala Trp Val Pro  
   50                  55                  60  
 Asp Pro Asp Thr Gly Tyr Tyr Arg Pro Gly Asn Glu Asp Lys Ala Ala  
   65                  70                  75                  80  
 Leu Asp Pro Val Glu Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser  
                   85                  90                  95  
 Arg Gln

<210> 29  
 <211> 490  
 <212> DNA  
 <213> Avicennia marina

<220>  
 <221> CDS  
 <222> (20)..(349)

<400> 29  
 tcggctgggc aaagaaggg atg gcg att cca tcg gaa att cgg gac ttt att 52  
                   Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile  
                   1                  5                  10  
 gct agc cgc aac aga tct ttg gtg atc gca tct cca aag gaa gat gag 100  
 Ala Ser Arg Asn Arg Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu  
                   15                  20                  25

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aaa att ctc cgc tca agg cag tgc acc gaa gaa ggg gcg cgt gca gga 148
Lys Ile Leu Arg Ser Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly
      30              35              40

gcc aaa gct gct gca gtt gct tgc gtt gcc agc gcc att ccc act ctg 196
Ala Lys Ala Ala Ala Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu
      45              50              55

gta gct gtt cga acg att ccg tgg gca aag gca aac ctc aac tat aca 244
Val Ala Val Arg Thr Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr
      60              65              70              75

gcc cag gca ctc att ata tct tct gca tcc ata gcg gca tac ttt atc 292
Ala Gln Ala Leu Ile Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile
      80              85              90

gct gct gac aaa acc atc tta gag tgc gca cgg aaa aat gca gag tac 340
Ala Ala Asp Lys Thr Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr
      95              100             105

aaa tcg gct taagatgatg tgtaagacaa tgtgctcagc ttgcaatgct 389
Lys Ser Ala
      110

tgccatgact tgtgtttatg tgtatttcaa gtttctgaaa ctagcatttt gattttgtgt 449

tccaatgcaa tgagcattat ggaaaaaaaa aaaaaaaaaa a 490

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&lt;210&gt; 30

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Avicennia marina

&lt;400&gt; 30

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Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile Ala Ser Arg Asn Arg
  1              5              10              15

Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu Lys Ile Leu Arg Ser
      20              25              30

Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly Ala Lys Ala Ala Ala
      35              40              45

Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu Val Ala Val Arg Thr
      50              55              60

Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr Ala Gln Ala Leu Ile
      65              70              75              80

Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile Ala Ala Asp Lys Thr
      85              90              95

Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr Lys Ser Ala
      100             105             110

```

<210> 31  
 <211> 592  
 <212> DNA  
 <213> Avicennia marina

<220>  
 <221> CDS  
 <222> (75)..(320)

<400> 31  
 gcagtcctcag ccttctctgct ctctctggtgc cttcaaattt gtgaatttct cgagtgctaa 60  
 aagattcagc caag atg cag aac gaa gag ggg caa aac atg gat ctc tac 110  
                   Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr  
                   1                  5                  10  
 atc ccc agg aaa tgc tct gcc acg aac agg ctg atc acc tcc aag gat 158  
 Ile Pro Arg Lys Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp  
                   15                  20                  25  
 cat gct tct gtc cag atc aat gtt ggg cac ttg gat gag aat ggc cga 206  
 His Ala Ser Val Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg  
                   30                  35                  40  
 tac act ggc caa tac tct acc ttt gct ctt tgt gga ttc atc cgt gct 254  
 Tyr Thr Gly Gln Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala  
                   45                  50                  55                  60  
 cag ggt gat gct gac agt gct ctt gat agg ctc tgg cag aaa aag aaa 302  
 Gln Gly Asp Ala Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys  
                   65                  70                  75  
 gtc gaa acc agg cag cag tgatcctgct caattcagca gtgaaagttt 350  
 Val Glu Thr Arg Gln Gln  
                   80  
 tttgggtttt gttctgtgtt gtgttattta tgcttttcca gaatcaattt ctgtactgga 410  
 ttgagtatta aaaatgtgga gctaaagggtt gggagacctg atgcctttgt tactcgagta 470  
 atcacaagta gatactgggc ttgtaatagc gtgataattg tgccttgctc ttgcctcatt 530  
 gactacgaat cagttatgtg attagacaat gttaatctcc aaaaaaaaaa aaaaaaaaaa 590  
 aa 592

<210> 32  
 <211> 82  
 <212> PRT  
 <213> Avicennia marina

<400> 32  
 Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr Ile Pro Arg Lys  
   1                  5                  10                  15  
 Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp His Ala Ser Val  
                   20                  25                  30



Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys Val Glu Thr Arg  
65 70 75 80

Gln Gln

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<210> 33
<211> 1806
<212> DNA
<213> Avicennia marina
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<220>
<221> CDS
<222> (362) .. (1552)
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<400>	33																					
tg	tga	agg	ta	aag	tct	acag	cat	attt	tcgc	gcc	gct	cg	tt	tg	att	ac	gtg	ttg	ctt	ttt	at	60
tt	gga	aatt	tt	gat	agc	gctg	agt	agc	cgat	gcc	gct	gg	ag	ggt	att	gtt	g	ttt	ta	gg	aa	120
tac	ggg	ttt	g	ttt	gatt	tcgc	agt	ttt	tact	g	tct	ctag	gg	t	ggg	cc	ctg	g	gct	tct	ggg	180
att	ttg	ggg	att	ta	atc	gctg	tcg	aac	ag	tt	tct	tg	gag	aa	a	act	c	ct	g	cat	at	240
at	ctg	att	ttg	ctg	acg	ag	aa	att	gata	cac	gg	t	atg	cg	g	ttt	g	cg	cc	aa		300
ag	a	act	ctc	g	agt	gct	cg	ct	ag	at	gt	gg	at	a	at	cc	g	g	ag			360
g	atg	tta	tca	ggg	tta	atg	aac	ttc	ctg	tgg	gcc	tgt	ttt	cgg	cca	agg						409
Met	Leu	Ser	Gly	Leu	Met	Asn	Phe	Leu	Trp	Ala	Cys	Phe	Arg	Pro	Arg							
1					5					10					15							
gcg	gat	cga	agt	gtt	cac	acg	ggt	tca	gat	gca	ggc	ggt	cgt	cag	gat							457
Ala	Asp	Arg	Ser	Val	His	Thr	Gly	Ser	Asp	Ala	Gly	Gly	Arg	Gln	Asp							
			20					25					30									
ggg	ctt	tta	tgg	tat	aag	gac	ttg	ggg	caa	cat	atc	aat	gga	gag	ttt							505
Gly	Leu	Ser	Leu	Trp	Tyr	Lys	Asp	Leu	Gly	Gln	His	Ile	Asn	Gly	Glu	Phe						
			35					40					45									
tca	atg	gct	gta	gtt	caa	gca	aat	aac	tta	cta	gag	gat	cag	agt	caa							553
Ser	Met	Ala	Val	Val	Gln	Ala	Asn	Asn	Leu	Leu	Glu	Asp	Gln	Ser	Gln							
			50				55					60										
ctt	gaa	tct	ggt	tgc	ctg	agc	ttg	agt	gat	tca	gga	caa	tat	ggc	act							601
Leu	Glu	Ser	Gly	Cys	Leu	Ser	Leu	Ser	Asp	Ser	Gly	Gln	Tyr	Gly	Thr							
			65			70				75					80							
ttt	gtg	ggg	att	tat	gat	gga	cat	gga	ggt	cct	gag	acc	tct	cgg	ttt							649
Phe	Val	Gly	Ile	Tyr	Asp	Gly	His	Gly	Gly	Pro	Glu	Thr	Ser	Arg	Phe							
				85					90					95								

atc aat gac cat ctc ttc caa cat ata aag aga ttc aca gct gag cat	697
Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His	
100 105 110	
caa tca atg tca gct gag gtc att cac aag gcc att caa gcg act gaa	745
Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu	
115 120 125	
gaa ggt ttt ttc tcg gtt gtt agc aga caa tgg tcc atg caa cca cag	793
Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln	
130 135 140	
att gca gca gtt ggc tct tgc tgc ctt gtt ggt gtc atc tgt agt ggc	841
Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly	
145 150 155 160	
act ctt tat gtt tcc aac ctt ggt gat tcc cgt gct gtt ctt ggg acg	889
Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr	
165 170 175	
ctt tcc aag gct aca ggg gaa gta cag gct act caa ctc tca aca gag	937
Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu	
180 185 190	
cat aat gca agt ttt gag tct gtg aga cgg gaa ctg cag tct ctg cac	985
His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His	
195 200 205	
cca gat gac tca cag att gtg gtt cta aag cat aat gta tgg cga gtg	1033
Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val	
210 215 220	
aag ggt ctt ata cag atc tca aga tca att gga gat gtg tat ttg aaa	1081
Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys	
225 230 235 240	
aag gct gaa ttc aac agg gag cct cta tat cag aaa ttt cga ctt cgt	1129
Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg	
245 250 255	
gaa gct ttc aaa aga cca att ttg agc tca gaa cca gaa act act gtg	1177
Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val	
260 265 270	
cac cag ctg ctg cct cat gat caa ttc att atc ttc gca tca gat ggc	1225
His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly	
275 280 285	
ctt tgg gag cac ctt tcc aac caa gaa gca gtt gat ctt gtt cag aaa	1273
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys	
290 295 300	
cat cca cac aat ggg att gct aga aga tta gta aaa gca gct ttg caa	1321
His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln	
305 310 315 320	

[illegible]

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<210> 34
<211> 397
<212> PRT
<213> Avicennia marina
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<400> 34
Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg
  1              5              10             15

Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp
      20              25             30

Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe
      35              40             45

Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln
      50              55             60

Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr
      65              70             75             80

Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe
      85              90             95

Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His
      100             105            110

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Gln	Ser	Met	Ser	Ala	Glu	Val	Ile	His	Lys	Ala	Ile	Gln	Ala	Thr	Glu	115	120	125
Glu	Gly	Phe	Phe	Ser	Val	Val	Ser	Arg	Gln	Trp	Ser	Met	Gln	Pro	Gln	130	135	140
Ile	Ala	Ala	Val	Gly	Ser	Cys	Cys	Leu	Val	Gly	Val	Ile	Cys	Ser	Gly	145	150	155
Thr	Leu	Tyr	Val	Ser	Asn	Leu	Gly	Asp	Ser	Arg	Ala	Val	Leu	Gly	Thr	165	170	175
Leu	Ser	Lys	Ala	Thr	Gly	Glu	Val	Gln	Ala	Thr	Gln	Leu	Ser	Thr	Glu	180	185	190
His	Asn	Ala	Ser	Phe	Glu	Ser	Val	Arg	Arg	Glu	Leu	Gln	Ser	Leu	His	195	200	205
Pro	Asp	Asp	Ser	Gln	Ile	Val	Val	Leu	Lys	His	Asn	Val	Trp	Arg	Val	210	215	220
Lys	Gly	Leu	Ile	Gln	Ile	Ser	Arg	Ser	Ile	Gly	Asp	Val	Tyr	Leu	Lys	225	230	235
Lys	Ala	Glu	Phe	Asn	Arg	Glu	Pro	Leu	Tyr	Gln	Lys	Phe	Arg	Leu	Arg	245	250	255
Glu	Ala	Phe	Lys	Arg	Pro	Ile	Leu	Ser	Ser	Glu	Pro	Glu	Thr	Thr	Val	260	265	270
His	Gln	Leu	Leu	Pro	His	Asp	Gln	Phe	Ile	Ile	Phe	Ala	Ser	Asp	Gly	275	280	285
Leu	Trp	Glu	His	Leu	Ser	Asn	Gln	Glu	Ala	Val	Asp	Leu	Val	Gln	Lys	290	295	300
His	Pro	His	Asn	Gly	Ile	Ala	Arg	Arg	Leu	Val	Lys	Ala	Ala	Leu	Gln	305	310	315
Glu	Ala	Ala	Lys	Lys	Arg	Glu	Met	Arg	Tyr	Ser	Asp	Leu	Lys	Lys	Ile	325	330	335
Asp	Arg	Gly	Val	Arg	Arg	His	Phe	His	Asp	Asp	Ile	Thr	Val	Val	Val	340	345	350
Val	Phe	Leu	Asp	Ser	His	Leu	Val	Ser	Arg	Ala	Ser	Ser	Val	Arg	Gly	355	360	365
Pro	Asn	Ile	Ser	Val	Lys	Gly	Gly	Gly	Ile	Ser	Leu	Pro	Pro	Asn	Ala	370	375	380
Leu	Ala	Pro	Cys	Ala	Thr	Pro	Thr	Glu	Pro	Val	Pro	Asn				385	390	395

&lt;210&gt; 35

&lt;211&gt; 743

&lt;212&gt; DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (1)..(420)

<400> 35

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cct gag cta gca cct aaa gat ggg gat ttc cgt ttc aat atc tct gag 48
Pro Glu Leu Ala Pro Lys Asp Gly Asp Phe Arg Phe Asn Ile Ser Glu
1 5 10 15

ctt gaa gct atg cta cca gct gga act gta gat cat gct gtt gaa agg 96
Leu Glu Ala Met Leu Pro Ala Gly Thr Val Asp His Ala Val Glu Arg
20 25 30

att tat caa gag atg ccg cgg tgg gaa gag act gtt tta ggt tcc agg 144
Ile Tyr Gln Glu Met Pro Arg Trp Glu Glu Thr Val Leu Gly Ser Arg
35 40 45

agc aga tat gag cat gtc att cag gca ctt gca gat aaa tac cct tca 192
Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser
50 55 60

gaa aat ttg ttg cta gtt acg cat ggt gaa ggt gtt ggg act tca gtt 240
Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val
65 70 75 80

gca acg ttt ttg aaa ggc gct gtt gtt tat gaa gta aag tat tgt gct 288
Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala
85 90 95

tat tca caa gca aca aga cgc atc agc tat gga gaa ggc gag tca ttt 336
Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe
100 105 110

act gct ggt acc ttt cag ttg gtc act gcc tca gac caa acc ggt att 384
Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile
115 120 125

ggt tac tac aca tct agc agc ttg tct gat ggt gta tgacttatcg 430
Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val
130 135 140

gaactcccgat gtttctgcat tctgaaagggt gctttttgat ttccgaataa ttcttcaaat 490

ccacatgtca gaagatccat tctttagggtc agatgtctat ctactgctcc cagccttgag 550

ctgctcatgg gtattggtgc ccttctatatt ttaggttagag tctttgagta agccttgcca 610

catcaaggcc tcagattatt gaatgtacaa cagaatagggt tgtagcttca ttggctagta 670

cagtgacctc tttcatgggt ctgaaacatc aatataaagg tttgaatggc aaaaaaaaaa 730
aaaaaaaaaa aaa 743

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<210> 36

<211> 140

&lt;212&gt; PRT

&lt;213&gt; Mesembryanthemum crystallinum

&lt;400&gt; 36

Pro Glu Leu Ala Pro Lys Asp Gly Asp Phe Arg Phe Asn Ile Ser Glu  
 1 5 10 15

Leu Glu Ala Met Leu Pro Ala Gly Thr Val Asp His Ala Val Glu Arg  
 20 25 30

Ile Tyr Gln Glu Met Pro Arg Trp Glu Glu Thr Val Leu Gly Ser Arg  
 35 40 45

Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser  
 50 55 60

Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val  
 65 70 75 80

Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala  
 85 90 95

Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe  
 100 105 110

Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile  
 115 120 125

Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val  
 130 135 140

&lt;210&gt; 37

&lt;211&gt; 348

&lt;212&gt; DNA

&lt;213&gt; Sueada japonica

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(246)

&lt;400&gt; 37

atc att gct ccc cta gct att ggt ttg atc gtt ggt gcc aac atc tta 48  
 Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu  
 1 5 10 15

gcc gga ggt gca ttt gat ggt gcc tca atg aac cct gcc gtc tct ttt 96  
 Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe  
 20 25 30

ggc ccc gcc gtg gtt agc tgg agc tgg gcc aac cac tgg gtc tac tgg 144  
 Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp  
 35 40 45

gca ggc cca ctc att ggt ggt gga ctt gct ggt ctc gtt tat gag ttt 192  
 Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe  
 50 55 60

atc ttt att ggt cac caa gag cca gct tcc gct gac tac cag aga ctc 240  
 Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu  
 65 70 75 80

tct gct taagaatttt aattctttgc cctagggaaa aatgtttcat gcatgtattt 296  
 Ser Ala

tggtatttttg ttgggtctaa aattttatga agggaaaaaa aaaaaaaaaa aa 348

<210> 38

<211> 82

<212> PRT

<213> Sueada japonica

<400> 38

Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu  
 1 5 10 15

Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe  
 20 25 30

Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp  
 35 40 45

Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe  
 50 55 60

Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu  
 65 70 75 80

Ser Ala

<210> 39

<211> 1602

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (1)..(1419)

<400> 39

cac acc gtt gat tta acc att gaa gct atg atg ctc gat tct caa gct 48  
 His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala  
 1 5 10 15

tct gat ctt gac aaa gaa gaa cgt cct gag att ctt tca atg ctt ccg 96  
 Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro  
 20 25 30

cct ctt gaa gga aaa tgc ctc ttg gaa ctt ggg gct ggt att ggt cgt 144  
 Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg  
 35 40 45

ttt act ggt gaa ttg gct gag aaa gct ggc cag gtt att gct ctg gat	192
Phe Thr Gly Glu Leu Ala Glu Lys Ala Gly Gln Val Ile Ala Leu Asp	
50 55 60	
ttc att gag agt gct atc aag aag aat gaa gta atc aat ggg cac tac	240
Phe Ile Glu Ser Ala Ile Lys Lys Asn Glu Val Ile Asn Gly His Tyr	
65 70 75 80	
aaa aat gtc aag ttt atg tgt gct gat gtg act tct ccc act ctc agt	288
Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr Ser Pro Thr Leu Ser	
85 90 95	
ttc cca cca cat tca ttg gat gtg ata ttc tcc aat tgg tta ctc atg	336
Phe Pro Pro His Ser Leu Asp Val Ile Phe Ser Asn Trp Leu Leu Met	
100 105 110	
tat ctt tct gat gaa gag gtg gaa aat ttg gtt gaa aga atg ttg aaa	384
Tyr Leu Ser Asp Glu Glu Val Glu Asn Leu Val Glu Arg Met Leu Lys	
115 120 125	
tgg ttg aag cca ggg ggt tac att ttc ttc aga gaa tct tgt ttc cat	432
Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His	
130 135 140	
caa tct ggg gat cac aaa cgc aaa agc aat ccc acc cac tac cgt gaa	480
Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu	
145 150 155 160	
cct agg ttc tac act aag gcc ttc aaa gag tgt cat ttg caa gat gga	528
Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly	
165 170 175	
tct gga aac tct tat gag ctc tcc cta ctt agc tgc aaa tgt att gga	576
Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly	
180 185 190	
gct tat gtc aga aac aag aaa aac cag aac cag att agt tgg ttg tgg	624
Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp	
195 200 205	
caa aaa gtt gat tct aag gat gat aag ggg ttc cag cga ttt ctg gat	672
Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp	
210 215 220	
act agc cag tac aag tgt aat agc att ctg cga tat gag cgt gta ttt	720
Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe	
225 230 235 240	
ggc cct ggt tat gtt agc act gga gga tat gaa acc acc aaa gag ttt	768
Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe	
245 250 255	
gtg tca atg ctg gac ttg aag cct ggc cag aag gtc ctg gat gtt ggt	816
Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly	
260 265 270	



tgt gga att ggt gga ggt gac ttt tac atg gcg gag acc ttt gat gtt	864
Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val	
275 280 285	
gag gtt gtt gga ttt gat ctc tcc gtt aat atg att tcc ttt gcc ctt	912
Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu	
290 295 300	
gag cgt tct att ggg ctt aaa tgt gct gtt gag ttt gag gta gca gat	960
Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp	
305 310 315 320	
tgc acc aag ata aac tac cct gat aac tct ttt gat gtc atc tat agc	1008
Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser	
325 330 335	
cgt gac acc att ctg cat att cag gac aag cct gcg ttg ttt aga tcc	1056
Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser	
340 345 350	
ttc tac aaa tgg ttg aag cca gga ggt aaa gtt cta atc agt gat tac	1104
Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr	
355 360 365	
tgc aag aaa gct ggt cca ccc tca cct gaa ttc gcc gct tac att aag	1152
Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys	
370 375 380	
cag agg gga tat gat ctc cat gat gta aag gaa tat ggg cag atg ctt	1200
Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu	
385 390 395 400	
aaa gat gct gga ttt gtt gat gtt ctt gcc gag gat aga act gag cag	1248
Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln	
405 410 415	
ttc att cga gtt cta cgg aag gaa cta gag act gtt gag aag gaa aag	1296
Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys	
420 425 430	
gat gtg ttc att agt gat ttc tct gag gag gat tac aat gac att gtt	1344
Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val	
435 440 445	
gga ggt tgg aat gat aag ttg cgg agg act gcc aag ggt gag caa cga	1392
Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg	
450 455 460	
tgg ggt ctg ttc gtt gcc aag aag aag tgaagaatca gttgccgcac	1439
Trp Gly Leu Phe Val Ala Lys Lys Lys	
465 470	
tggcactgtc gatttcctag tattaatctt caatgttttc atgtaatgta cttctacatg	1499
taaaattgcc aataagttgc atttcgcaga ctgtaagatg attaatacata ttttatcttt	1559
taattaatca tggatttatg caaaaaaaaaa aaaaaaaaaa aaa	1602

<210> 40  
 <211> 473  
 <212> PRT  
 <213> Sueada japonica

<400> 40

His	Thr	Val	Asp	Leu	Thr	Ile	Glu	Ala	Met	Met	Leu	Asp	Ser	Gln	Ala
1				5					10					15	
Ser	Asp	Leu	Asp	Lys	Glu	Glu	Arg	Pro	Glu	Ile	Leu	Ser	Met	Leu	Pro
			20					25					30		
Pro	Leu	Glu	Gly	Lys	Cys	Leu	Leu	Glu	Leu	Gly	Ala	Gly	Ile	Gly	Arg
		35					40					45			
Phe	Thr	Gly	Glu	Leu	Ala	Glu	Lys	Ala	Gly	Gln	Val	Ile	Ala	Leu	Asp
	50					55					60				
Phe	Ile	Glu	Ser	Ala	Ile	Lys	Lys	Asn	Glu	Val	Ile	Asn	Gly	His	Tyr
65					70					75					80
Lys	Asn	Val	Lys	Phe	Met	Cys	Ala	Asp	Val	Thr	Ser	Pro	Thr	Leu	Ser
				85					90					95	
Phe	Pro	Pro	His	Ser	Leu	Asp	Val	Ile	Phe	Ser	Asn	Trp	Leu	Leu	Met
			100					105					110		
Tyr	Leu	Ser	Asp	Glu	Glu	Val	Glu	Asn	Leu	Val	Glu	Arg	Met	Leu	Lys
		115					120					125			
Trp	Leu	Lys	Pro	Gly	Gly	Tyr	Ile	Phe	Phe	Arg	Glu	Ser	Cys	Phe	His
	130					135					140				
Gln	Ser	Gly	Asp	His	Lys	Arg	Lys	Ser	Asn	Pro	Thr	His	Tyr	Arg	Glu
145					150					155					160
Pro	Arg	Phe	Tyr	Thr	Lys	Ala	Phe	Lys	Glu	Cys	His	Leu	Gln	Asp	Gly
				165					170					175	
Ser	Gly	Asn	Ser	Tyr	Glu	Leu	Ser	Leu	Leu	Ser	Cys	Lys	Cys	Ile	Gly
			180					185					190		
Ala	Tyr	Val	Arg	Asn	Lys	Lys	Asn	Gln	Asn	Gln	Ile	Ser	Trp	Leu	Trp
		195					200					205			
Gln	Lys	Val	Asp	Ser	Lys	Asp	Asp	Lys	Gly	Phe	Gln	Arg	Phe	Leu	Asp
	210					215					220				
Thr	Ser	Gln	Tyr	Lys	Cys	Asn	Ser	Ile	Leu	Arg	Tyr	Glu	Arg	Val	Phe
225					230					235					240
Gly	Pro	Gly	Tyr	Val	Ser	Thr	Gly	Gly	Tyr	Glu	Thr	Thr	Lys	Glu	Phe
				245					250					255	
Val	Ser	Met	Leu	Asp	Leu	Lys	Pro	Gly	Gln	Lys	Val	Leu	Asp	Val	Gly
			260					265					270		

Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val  
           275                                  280                                  285  
 Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu  
           290                                  295                                  300  
 Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp  
   305                                  310                                  315                                  320  
 Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser  
                                   325                                  330                                  335  
 Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser  
                                   340                                  345                                  350  
 Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr  
                                   355                                  360                                  365  
 Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys  
           370                                  375                                  380  
 Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu  
   385                                  390                                  395                                  400  
 Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln  
                                   405                                  410                                  415  
 Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys  
                                   420                                  425                                  430  
 Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val  
                                   435                                  440                                  445  
 Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg  
           450                                  455                                  460  
 Trp Gly Leu Phe Val Ala Lys Lys Lys  
   465                                  470

&lt;210&gt; 41

&lt;211&gt; 1251

&lt;212&gt; DNA

&lt;213&gt; Salsola komarovii

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(933)

&lt;400&gt; 41

cag cca ttt ggc aca att aat gga tca ctt cgt gtt act gta caa ggt 48  
 Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly  
   1                                  5                                  10                                  15

gag gtc att gaa caa tct ttt gga gag gag cac ttg tgt ttt aga aca 96  
 Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr  
                                   20                                  25                                  30

tta	cag	cgg	tac	aca	gct	gcc	aca	ctt	gag	cat	gga	atg	cat	cca	cca	144
Leu	Gln	Arg	Tyr	Thr	Ala	Ala	Thr	Leu	Glu	His	Gly	Met	His	Pro	Pro	
		35					40					45				
atc	tct	cct	aaa	cca	gaa	tgg	cgt	gca	ctt	ttg	gac	gag	atg	gct	gtt	192
Ile	Ser	Pro	Lys	Pro	Glu	Trp	Arg	Ala	Leu	Leu	Asp	Glu	Met	Ala	Val	
		50				55					60					
gtt	gcc	acc	aag	gaa	tac	cgc	tct	gtt	gtt	ttt	cat	gag	cct	cgc	ttt	240
Val	Ala	Thr	Lys	Glu	Tyr	Arg	Ser	Val	Val	Phe	His	Glu	Pro	Arg	Phe	
	65				70					75					80	
gtc	gag	tac	ttc	cgc	agt	gct	aca	cca	gag	aca	gag	tat	ggg	cgt	atg	288
Val	Glu	Tyr	Phe	Arg	Ser	Ala	Thr	Pro	Glu	Thr	Glu	Tyr	Gly	Arg	Met	
				85				90						95		
aat	att	gga	agc	cgt	cct	gca	aag	aga	aag	cca	gga	gga	gga	att	gaa	336
Asn	Ile	Gly	Ser	Arg	Pro	Ala	Lys	Arg	Lys	Pro	Gly	Gly	Gly	Ile	Glu	
			100					105					110			
act	ctg	cgt	gca	att	cct	tgg	ata	ttt	tcg	tgg	aca	caa	acc	agg	ttt	384
Thr	Leu	Arg	Ala	Ile	Pro	Trp	Ile	Phe	Ser	Trp	Thr	Gln	Thr	Arg	Phe	
		115					120					125				
cat	tta	cct	gtg	tgg	ctt	ggg	gtt	gga	gca	gct	ttt	aag	cat	gcc	ctt	432
His	Leu	Pro	Val	Trp	Leu	Gly	Val	Gly	Ala	Ala	Phe	Lys	His	Ala	Leu	
	130					135					140					
gac	aag	gac	att	aag	aat	ctt	tcg	ata	ctc	aag	gcc	atg	tat	aat	gag	480
Asp	Lys	Asp	Ile	Lys	Asn	Leu	Ser	Ile	Leu	Lys	Ala	Met	Tyr	Asn	Glu	
	145				150					155					160	
tgg	ccg	ttc	ttc	aga	gtg	act	att	gat	ctc	tta	gaa	atg	gtt	ttc	act	528
Trp	Pro	Phe	Phe	Arg	Val	Thr	Ile	Asp	Leu	Leu	Glu	Met	Val	Phe	Thr	
				165					170					175		
aaa	gga	gac	cct	gga	att	gct	gct	tta	tat	gac	aag	ctt	ctg	gtg	gca	576
Lys	Gly	Asp	Pro	Gly	Ile	Ala	Ala	Leu	Tyr	Asp	Lys	Leu	Leu	Val	Ala	
			180					185					190			
gag	gat	ttg	aag	ccc	ttt	ggg	gaa	aag	ttg	agg	aaa	agt	ttc	gaa	gat	624
Glu	Asp	Leu	Lys	Pro	Phe	Gly	Glu	Lys	Leu	Arg	Lys	Ser	Phe	Glu	Asp	
		195					200				205					
acc	aaa	ctc	ctt	ctc	ctt	aag	gtt	gct	ggg	cac	aag	gag	tta	ctg	gaa	672
Thr	Lys	Leu	Leu	Leu	Leu	Lys	Val	Ala	Gly	His	Lys	Glu	Leu	Leu	Glu	
		210				215					220					
gga	gat	cct	tac	ttg	aaa	cag	aga	ctc	cga	ctt	cgt	gat	cct	tac	att	720
Gly	Asp	Pro	Tyr	Leu	Lys	Gln	Arg	Leu	Arg	Leu	Arg	Asp	Pro	Tyr	Ile	
	225				230					235					240	
aca	acc	ctt	aat	gtt	ttc	caa	gca	tat	act	ctg	aag	cgg	atc	cgt	gat	768
Thr	Thr	Leu	Asn	Val	Phe	Gln	Ala	Tyr	Thr	Leu	Lys	Arg	Ile	Arg	Asp	
				245					250					255		

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ccc aat ttc cat gta gct gaa ggg cca cac tta tcc aag gaa gta ttg      816
Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu
      260                      265                      270

gaa tca aac aat gct gag ctt gtg aag ctc aat cct act agt gag tat      864
Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr
      275                      280                      285

cct cct ggc ctt gag gac acc ctt atc ttg acc atg aag ggt att gct      912
Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala
      290                      295                      300

gct ggc atg cag aac acc ggt taactgacac gtgttgacag tctattgcaa      963
Ala Gly Met Gln Asn Thr Gly
      305                      310

ctattcctca actccttctg gtttggggat cggggctcgg agatagccat cgttggtgat 1023

gtgctgtatg agcacctaatt tgtattcaaa gtctgtatct caagtctatt gtatttgtat 1083

tttgttcttc tgtatgtttt tgttatttct acttatgggt gggttgtgtc acttgtgact 1143

aatacccgac tgtgtaataa atggttggtg tactgatgaa cagtttggtt tcttctacgt 1203

gagttatatt gatgagttta tcttttatta aaaaaaaaaa aaaaaaaaaa      1251

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<210> 42
<211> 311
<212> PRT
<213> Salsola komarovii

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<400> 42
Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly
  1                      5                      10                      15

Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr
      20                      25                      30

Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro
      35                      40                      45

Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val
      50                      55                      60

Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe
      65                      70                      75                      80

Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met
      85                      90                      95

Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Gly Ile Glu
      100                      105                      110

Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe
      115                      120                      125

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His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu  
 130 135 140  
 Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu  
 145 150 155 160  
 Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr  
 165 170 175  
 Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala  
 180 185 190  
 Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp  
 195 200 205  
 Thr Lys Leu Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu  
 210 215 220  
 Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile  
 225 230 235 240  
 Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp  
 245 250 255  
 Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu  
 260 265 270  
 Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr  
 275 280 285  
 Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala  
 290 295 300  
 Ala Gly Met Gln Asn Thr Gly  
 305 310

<210> 43  
 <211> 637  
 <212> DNA  
 <213> Avicennia marina

<220>  
 <221> CDS  
 <222> (1)..(339)

<400> 43  
 caa tac ttg gta aat gaa gtg aag aaa act gtt cag ggg cgt gct caa 48  
 Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln  
 1 5 10 15  
 ctt ggt gtg gaa gca ttt gct gat gcg ctt ctt gtg gtt cca aag acg 96  
 Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Val Val Pro Lys Thr  
 20 25 30  
 ctt gcc gag aac tct ggc ctt gat acc cag gat ttg att att gaa ctt 144  
 Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu  
 35 40 45

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acg gga gaa tat gaa aaa ggg aat gtg gta gga ctt aat cta cac aca 192
Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr
   50               55               60

gga gaa cct ata gat cct caa atg gag ggt atc ttt gac aat tat tcc 240
Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser
   65               70               75               80

gtg aag cgt cag atc ata aac tca ggc ccc gtt att gca tct cag ctg 288
Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu
               85               90               95

cta ctt gtc gac gag gtt att cgt gct ggt cgt aac atg cgt aaa ccg 336
Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro
               100               105               110

aat tagctttcac cctagttttt gtgatgttgg tgaagatggt aattttattt 389
Asn

aggtagggtc atggttcctt ttgtttagcc taagcactat gtattcattg ccacttgaga 449

tttgaatttt gatcatcagg cggttgaact tttcgctgtg tacaaattgc accagaaatt 509

attcgaccat gggatgcat ctacttgtgt tgtacctgac ttggctaagt tatttgaaga 569

tacactctgt gctcagcaaa gaattggaaa aaaaggaatt gatttcatca aaaaaaaaaa 629
aaaaaaaaa 637

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<210> 44
<211> 113
<212> PRT
<213> Avicennia marina

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<400> 44
Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln
   1               5               10               15

Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr
               20               25               30

Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu
               35               40               45

Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr
   50               55               60

Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser
   65               70               75               80

Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu
               85               90               95

Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro
               100               105               110

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Asn

<210> 45  
 <211> 741  
 <212> DNA  
 <213> *Avicennia marina*

<220>  
 <221> CDS  
 <222> (3)..(293)

<400> 45  
 aa gag atc aat tgt ctt gaa tgg gag aac ttt gct ttc cat ccc agc 47  
   Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser  
     1                  5                  10                  15  
 cca ctc att gtt ctt gtt ttt gaa aga tac aac agg gca agt gat aac 95  
   Pro Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn  
                   20                  25                  30  
 tgg aaa gct ttg aag gag ttg gaa aag gcg gca gaa gtt tac tgg aag 143  
   Trp Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys  
                   35                  40                  45  
 gca aaa gat cga ctg cct cct cgg acg gtc aag ata gat ata aac atc 191  
   Ala Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile  
                   50                  55                  60  
 gaa agg gat tta gca tat gca ctc aag gtt aaa gaa tgc ccg cag ata 239  
   Glu Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile  
                   65                  70                  75  
 ctg ttc tta cgc gga aac agg ata tta tac aga gag aaa ggt agc cca 287  
   Leu Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro  
     80                  85                  90                  95  
 ttt ctc tgatattgca tgtacatcag atctttcaat ctgcaccaga accaattgag 343  
   Phe Leu  
 tttaccatca tttccagaaa ttagatcatc ggatgaattg gttcagatga tcgcgcattt 403  
 ctattacaat gcaaaaaagc cttcgtgcat cgatgatgca gctttctctt caccacatca 463  
 ctgaagggtga ggttgtcaaa tggaatccag catcagtcac tagggaggac tgaagctgta 523  
 cggagggaag tggttttaaatt tcagattgga tctttgaagt gggcagtggt gattgaaacg 583  
 ccaaaagtctt ctgaggaata accttggttg gattttgcag tgaactgtag taactttctc 643  
 gcatgtaaaa ctagactttc atcaatcaac caccaaccct tttatgtata tgaaacctat 703  
 gaggttgaaa tttctagtta aaaaaaaaaa aaaaaaaaaa 741

<210> 46  
 <211> 97  
 <212> PRT



<213> Avicennia marina

<400> 46

Glu	Ile	Asn	Cys	Leu	Glu	Trp	Glu	Asn	Phe	Ala	Phe	His	Pro	Ser	Pro		
1				5					10					15			
Leu	Ile	Val	Leu	Val	Phe	Glu	Arg	Tyr	Asn	Arg	Ala	Ser	Asp	Asn	Trp		
			20				25						30				
Lys	Ala	Leu	Lys	Glu	Leu	Glu	Lys	Ala	Ala	Glu	Val	Tyr	Trp	Lys	Ala		
		35					40					45					
Lys	Asp	Arg	Leu	Pro	Pro	Arg	Thr	Val	Lys	Ile	Asp	Ile	Asn	Ile	Glu		
	50					55					60						
Arg	Asp	Leu	Ala	Tyr	Ala	Leu	Lys	Val	Lys	Glu	Cys	Pro	Gln	Ile	Leu		
	65				70					75					80		
Phe	Leu	Arg	Gly	Asn	Arg	Ile	Leu	Tyr	Arg	Glu	Lys	Gly	Ser	Pro	Phe		
				85				90						95			

Leu

<210> 47

<211> 983

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (1)..(762)

<400> 47

atg	ttc	ctt	cat	cac	cac	ttt	tca	tct	tca	tct	tct	tct	ttt	ctt	ctt		48
Met	Phe	Leu	His	His	His	Phe	Ser	Ser	Ser	Ser	Ser	Ser	Phe	Leu	Leu		
1				5					10					15			
ctc	ttc	ttc	tct	ctc	cta	ata	ttc	ctt	tca	tct	gct	aat	ctt	tat	cat		96
Leu	Phe	Phe	Ser	Leu	Leu	Ile	Phe	Leu	Ser	Ser	Ala	Asn	Leu	Tyr	His		
			20					25					30				
cag	aat	caa	gga	tct	tgt	agt	gac	ttt	gaa	tca	gaa	cca	tca	atg	gct		144
Gln	Asn	Gln	Gly	Ser	Cys	Ser	Asp	Phe	Glu	Ser	Glu	Pro	Ser	Met	Ala		
		35					40					45					
act	ctt	ggt	gga	ttg	cgc	gaa	tcc	cat	ggt	gct	tct	aat	gat	gct	gag		192
Thr	Leu	Gly	Gly	Leu	Arg	Glu	Ser	His	Gly	Ala	Ser	Asn	Asp	Ala	Glu		
	50					55				60							
att	gaa	acc	ctt	gct	cgc	ttt	gct	gtt	gat	gaa	cac	aac	aaa	aaa	gag		240
Ile	Glu	Thr	Leu	Ala	Arg	Phe	Ala	Val	Asp	Glu	His	Asn	Lys	Lys	Glu		
	65				70				75						80		
aat	gca	ttg	ttg	gag	ttt	gca	agg	gtt	gta	aag	gca	aag	gaa	cag	gtg		288
Asn	Ala	Leu	Leu	Glu	Phe	Ala	Arg	Val	Val	Lys	Ala	Lys	Glu	Gln	Val		
				85				90						95			

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gtt gcg ggt aca ttg cat cac ttc act atc gaa gca att gaa gcg ggc 336
Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly
      100      105      110

aag aag aag ctc tac gaa gcg aag gtg tgg gtg aag cca tgg atg aac 384
Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn
      115      120      125

ttt aag gag ctg cag gaa ttt aag cat gct gat gaa tcc cct tca atc 432
Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile
      130      135      140

act cct tcc gac ctc ggc gct aat aga gaa ggg cat tct gga gga tgg 480
Thr Pro Ser Asp Leu Gly Ala Asn Arg Glu Gly His Ser Gly Gly Trp
      145      150      155      160

aaa gat gtg cct gtc cat gac cct gaa gtg caa aat gca gca aat cat 528
Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His
      165      170      175

gct ctt aag acc ttg caa caa aga tcc aac tcc tta ttt cct tat gaa 576
Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu
      180      185      190

ctg cag gaa gtt gct cat gct agg gct gag gtt ctg gaa gac act gcg 624
Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala
      195      200      205

aag ttt aac ctg cac ctc aag gtg aag aga gga aac aag gat gag ttt 672
Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe
      210      215      220

ttc aat gtg gag gtg cac aaa aac agc gaa gga aac tac aac ctt aat 720
Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn
      225      230      235      240

cag atg ggg aac gtt gag ccc gag gtt gag aaa agt agt gtt 762
Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val
      245      250

tagactcggt gaggggtgttg taagtactcg ttcgtaactt ttctgatggt caggcaagta 822

tgtagtaagg actagactac tagtactagt aagtacagct gacttggttt gagtaaaata 882

acctcgactt tggttgcacc atcatatctt gtatgtttat ggctttgtca atgtattgta 942

agtgaagatt gtttgcttga tctaaaaaaaa aaaaaaaaaa a 983

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&lt;210&gt; 48

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Salsola komarovii

&lt;400&gt; 48

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Met Phe Leu His His His Phe Ser Ser Ser Ser Ser Ser Phe Leu Leu
  1           5           10           15

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Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His  
                   20                  25                  30  
 Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala  
                   35                  40                  45  
 Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu  
           50                  55                  60  
 Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu  
       65                  70                  75                  80  
 Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val  
                   85                  90                  95  
 Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly  
                   100                  105                  110  
 Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn  
           115                  120                  125  
 Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile  
       130                  135                  140  
 Thr Pro Ser Asp Leu Gly Ala Asn Arg Glu Gly His Ser Gly Gly Trp  
   145                  150                  155                  160  
 Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His  
                   165                  170                  175  
 Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu  
                   180                  185                  190  
 Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala  
       195                  200                  205  
 Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe  
       210                  215                  220  
 Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn  
   225                  230                  235                  240  
 Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val  
                   245                  250

<210> 49

<211> 543

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (3)..(389)

&lt;400&gt; 49

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aa aat aag gtt gac tta gct cga gat ttc acc ttc ata gac gac gtc 47
  Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val
    1             5             10             15

gta aag ggg tgc tta ggt tca ctg gat tct tcc ggt aag agt acc ggt 95
Val Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly
          20             25             30

agc ggc ggt aaa aaa cgt ggg ccc gct ccg tac aga atc tac aac ttg 143
Ser Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu
          35             40             45

ggg aac act caa ccg gtc act gta ccg aca ctt gtc ggt atc cta gag 191
Gly Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu
          50             55             60

aag cat ctc aaa gtt aag gcc aag aag aat gtg gtt gag atg ccc gga 239
Lys His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly
          65             70             75

aat ggt gac gtg ccc ttc aca cat gcg aat atc tct ttg gcc cga aaa 287
Asn Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys
          80             85             90             95

gat ttc ggg tat aaa ccc act acc gat ttg caa acc ggg ttg aaa aag 335
Asp Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys
          100             105             110

ttt gtt aga tgg tat ctc act tat tac ggc tac aac aac ggc aag cct 383
Phe Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro
          115             120             125

gta aat taatatataa atataagtaa tattttttttt ctctttttttt ataaattaca 439
Val Asn

gaattattttt ttttgggtgg tttatgaatt ttgttgata atatggggat tcttttttttc 499

taaattgggaa aaataagaat ccaaggaaaa aaaaaaaaaa aaaa 543

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&lt;210&gt; 50

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Salsola komarovii

&lt;400&gt; 50

```

Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val Val
  1             5             10             15

Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly Ser
          20             25             30

Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu Gly
          35             40             45

Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu Lys
          50             55             60

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His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly Asn  
 65 70 75 80  
 Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys Asp  
 85 90 95  
 Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys Phe  
 100 105 110  
 Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro Val  
 115 120 125

Asn

<210> 51  
 <211> 1219  
 <212> DNA  
 <213> Sueada japonica

<220>  
 <221> CDS  
 <222> (2)..(871)

<400> 51  
 c aca gga gca aac aaa gga ata gga ctt gaa cta tgc aaa caa cta gct 49  
 Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala  
 1 5 10 15  
 gct aaa gga gtt gta gta gtt ctc act tct aga gat gga aaa aga ggc 97  
 Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly  
 20 25 30  
 tta caa gct cat gaa aat ctc att aaa tct gga att aat cct gaa aat 145  
 Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn  
 35 40 45  
 ctt cac ttt cat cag ctc gat gtt act gac atc act agt att gct gct 193  
 Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala  
 50 55 60  
 att gct ggt ttc atc aat tcc aaa ttc ggc aaa ctt gat atc ctg gtg 241  
 Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val  
 65 70 75 80  
 aac aat gct gga att att gga gat atg gtt aac ttt gat gct tta ata 289  
 Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile  
 85 90 95  
 gca gca gga ttt ggc act cca aga gaa cag atc aat ctt gag gac agt 337  
 Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser  
 100 105 110  
 ccc ggg aca gta aca cag aca tat gag ctt acg aaa gaa tgc tta caa 385  
 Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln  
 115 120 125

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aca aat tat tat gga gcg aaa aga acc gtt gaa gct ttg ctt ccg ctt 433
Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu
130 135 140

ctc aag tta tcc gat tct cca agg att gtc aat gtc tcc tct ttt cta 481
Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu
145 150 155 160

gga agg ttg acg tat ata cca aat gag acg atc aga ggg gtc cta aga 529
Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg
165 170 175

gat gcc gag agc ctt aca gaa gaa cga ata gat gag att ctg aat gac 577
Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp
180 185 190

atg ctg agg gac ttc aaa gac tgt tca ttc aaa gag aag gga tgg cct 625
Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro
195 200 205

aaa aat ctg gca gcc tat ata gtt tca aag gcg gcc ttg agt gca tac 673
Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr
210 215 220

aca aga ata ctg gct aag aaa tac cca tca atc atg atc aac tgt att 721
Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile
225 230 235 240

tgc cct ggc ttt gtc aaa act gac atc aat gga aac aca gga cac ttg 769
Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu
245 250 255

ccg gtt gaa gaa ggt gca gcg agt ctg gca agg tta gcg ttg atg ccc 817
Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro
260 265 270

caa att tta cct tct gga cta ttc ttt cag aga act gaa gtt tct tcg 865
Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser
275 280 285

ttt gaa taaaacaatt tgctattca aaccaacacc acatatctat gaagtttcca 921
Phe Glu
290

ttttaggca tctttacgaa aaaaataaga catctgcaat actgttactg gaaaatgcaa 981

tgtacttttt tcatgtatgc atggcgagcgt tatttattct gactgcaaca ataagattct 1041

gttcttttcaa ggcactctaa ggaatgctga tgtaccgttc tcaaacaagc agacaagtag 1101

acacgtttga ttgtcatgtc ttcattcgta caatcatttt gtgtttgtat gttgagcatg 1161

tttaactaat tacaagagtg taattaagat caactttttat aaaaaaaaaa aaaaaaaaaa 1219

<210> 52
<211> 290
<212> PRT

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&lt;213&gt; Sueada japonica

&lt;400&gt; 52

Thr	Gly	Ala	Asn	Lys	Gly	Ile	Gly	Leu	Glu	Leu	Cys	Lys	Gln	Leu	Ala	1	5	10	15
Ala	Lys	Gly	Val	Val	Val	Val	Leu	Thr	Ser	Arg	Asp	Gly	Lys	Arg	Gly	20	25	30	
Leu	Gln	Ala	His	Glu	Asn	Leu	Ile	Lys	Ser	Gly	Ile	Asn	Pro	Glu	Asn	35	40	45	
Leu	His	Phe	His	Gln	Leu	Asp	Val	Thr	Asp	Ile	Thr	Ser	Ile	Ala	Ala	50	55	60	
Ile	Ala	Gly	Phe	Ile	Asn	Ser	Lys	Phe	Gly	Lys	Leu	Asp	Ile	Leu	Val	65	70	75	80
Asn	Asn	Ala	Gly	Ile	Ile	Gly	Asp	Met	Val	Asn	Phe	Asp	Ala	Leu	Ile	85	90	95	
Ala	Ala	Gly	Phe	Gly	Thr	Pro	Arg	Glu	Gln	Ile	Asn	Leu	Glu	Asp	Ser	100	105	110	
Pro	Gly	Thr	Val	Thr	Gln	Thr	Tyr	Glu	Leu	Thr	Lys	Glu	Cys	Leu	Gln	115	120	125	
Thr	Asn	Tyr	Tyr	Gly	Ala	Lys	Arg	Thr	Val	Glu	Ala	Leu	Leu	Pro	Leu	130	135	140	
Leu	Lys	Leu	Ser	Asp	Ser	Pro	Arg	Ile	Val	Asn	Val	Ser	Ser	Phe	Leu	145	150	155	160
Gly	Arg	Leu	Thr	Tyr	Ile	Pro	Asn	Glu	Thr	Ile	Arg	Gly	Val	Leu	Arg	165	170	175	
Asp	Ala	Glu	Ser	Leu	Thr	Glu	Glu	Arg	Ile	Asp	Glu	Ile	Leu	Asn	Asp	180	185	190	
Met	Leu	Arg	Asp	Phe	Lys	Asp	Cys	Ser	Phe	Lys	Glu	Lys	Gly	Trp	Pro	195	200	205	
Lys	Asn	Leu	Ala	Ala	Tyr	Ile	Val	Ser	Lys	Ala	Ala	Leu	Ser	Ala	Tyr	210	215	220	
Thr	Arg	Ile	Leu	Ala	Lys	Lys	Tyr	Pro	Ser	Ile	Met	Ile	Asn	Cys	Ile	225	230	235	240
Cys	Pro	Gly	Phe	Val	Lys	Thr	Asp	Ile	Asn	Gly	Asn	Thr	Gly	His	Leu	245	250	255	
Pro	Val	Glu	Glu	Gly	Ala	Ala	Ser	Leu	Ala	Arg	Leu	Ala	Leu	Met	Pro	260	265	270	
Gln	Ile	Leu	Pro	Ser	Gly	Leu	Phe	Phe	Gln	Arg	Thr	Glu	Val	Ser	Ser	275	280	285	

Phe Glu  
290

<210> 53  
<211> 1148  
<212> DNA  
<213> Sueada japonica

<220>  
<221> CDS  
<222> (3)..(848)

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<400> 53
ga agc agg ccg gat atc cat gtt gaa caa gct cat tca gat gat att 47
  Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile
    1             5             10             15

act ggg ttg aaa ttc tca tgt gat ggt cgt cat ctg ttg tct aga agt 95
Thr Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser
          20             25             30

ttt gat tgc aca ctt aag gtt tgg gac ttg cgc caa atg aag cgg tct 143
Phe Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser
          35             40             45

ctt aag gtg ttt gat gaa tta cca aat cac tat gct caa acg aat gtc 191
Leu Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val
    50             55             60

tca ttt agt cca gat gag cag ctc atc ttg act ggt aca tct gta gaa 239
Ser Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu
    65             70             75

agg gat agc cca act gga gga ttg ttg tgc ttt tat gat cgg gaa aaa 287
Arg Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys
    80             85             90             95

ctt gaa cta gta tca aaa gtt ggc att tct cct act tgc agt gtt gtg 335
Leu Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val
          100             105             110

caa tgt gcc tgg cac cca agg ctg aat cag gtt ttt gcc act gct gga 383
Gln Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly
          115             120             125

aat aaa agc caa gga ggt aca cat gta ctc tat gat cca acc atg agt 431
Asn Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser
          130             135             140

gag aga ggt gct ctt gtg tgt gtt gct cgt gca cca agg atg aaa tca 479
Glu Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser
          145             150             155

gtg gat gat ttt gag gtg cag ccg gtt ata cat aac cct cac gca ctt 527
Val Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu
          160             165             170             175

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ccc ttg ttc aga gat cag cca agc cgc aaa cgt caa aga gag aag att 575
Pro Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile
                                180                                185                                190

ctg aag gac cca ata aaa tcc cac aaa cca gag ctt cct atg tca gga 623
Leu Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly
                                195                                200                                205

cct ggc cat ggt ggc aga act ggt aca tca tcg ggt agt ttg tta aca 671
Pro Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr
                                210                                215                                220

caa tat ctc ctc aag caa ggg ggc atg ttg aaa gag aca tgg atg gat 719
Gln Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp
                                225                                230                                235

gaa gat ccc aga gaa gct att ctc aag tat gct gat gct gca gaa aag 767
Glu Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys
240                                245                                250                                255

gat cca aag ttt att gcc ccg gct tat gct gag act cag ccc aag cca 815
Asp Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro
                                260                                265                                270

gtc ttt gag gat tct gat aag gaa gat gaa gaa taattcatct tttgcagtgg 868
Val Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu
                                275                                280

ttggattaat ttaatttgag aatattatac tgtgtatatt aatagccaat ttttcaggcg 928

aatgatatgc ttctcacatt acatgctgag ttttatttgc tgctacagat tgtagatgaa 988

taggttaatg taaacacaag catagagatt agaatataga aatgattctg tatccaaaac 1048

acaattttat caccagatgg tatcaaaaagc tgtattgact gttgagtaat gtcattaacc 1108

acttttcttc cccaaaaaaa aaaaaaaaaa aaaaaaaaaa 1148

<210> 54
<211> 282
<212> PRT
<213> Sueada japonica

<400> 54
Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile Thr
 1          5          10          15

Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser Phe
                                20          25          30

Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser Leu
 35          40          45

Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val Ser
 50          55          60

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Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu Arg  
 65 70 75 80  
 Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys Leu  
 85 90 95  
 Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val Gln  
 100 105 110  
 Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly Asn  
 115 120 125  
 Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser Glu  
 130 135 140  
 Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser Val  
 145 150 155 160  
 Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu Pro  
 165 170 175  
 Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile Leu  
 180 185 190  
 Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly Pro  
 195 200 205  
 Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr Gln  
 210 215 220  
 Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp Glu  
 225 230 235 240  
 Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys Asp  
 245 250 255  
 Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro Val  
 260 265 270  
 Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu  
 275 280

<210> 55  
 <211> 1193  
 <212> DNA  
 <213> Avicennia marina

<220>  
 <221> CDS  
 <222> (3)..(815)

<400> 55  
 gt gca cct gag tta ctt ctt gga gca aag cat tat aca agt gct gtt 47  
 Ala Pro Glu Leu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val  
 1 5 10 15

gac atg tgg gct gtg ggc tgc att ttt gct gag ctt ctg act cta aag	95
Asp Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys	
20 25 30	
cca cta ttt caa ggg caa gaa gta aaa ggg act tct aat cca ttt cag	143
Pro Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln	
35 40 45	
ctt gat caa ctt gac aaa atc ttt aag gtc cta ggt cat ccc acg caa	191
Leu Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln	
50 55 60	
gaa aag tgg ccc aca cta gcg aat ctt cca cat tgg cag tct gat gtg	239
Glu Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val	
65 70 75	
caa cgt atc caa ggg ctc aaa tac gac aat act gga ctt tac aat gtt	287
Gln Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val	
80 85 90 95	
gtt cat ctc tcc ccc aaa aat cca gca tat gac ctt ctc tca aag atg	335
Val His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met	
100 105 110	
ctt gag tat gat cct aga aaa aga ata aca gct aca caa gct ctt gag	383
Leu Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu	
115 120 125	
cat gag tat ttt cgc atg gaa cct ttg ccg gga cgc aac gct ctg gta	431
His Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val	
130 135 140	
cca cca cag cct ggg gag aaa att gtg aac tac cca aca cga cca gtg	479
Pro Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val	
145 150 155	
gac aca aat act gat att gaa gga aca atc agc ctc cag ccc tct caa	527
Asp Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln	
160 165 170 175	
ccg gta tca tct ggg aat tct gtg tct ggg gcc cta gcc ggt cct cat	575
Pro Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His	
180 185 190	
gta atg caa aat aga tcc atg cct cgg cca atg ccc atg gtt ggc gtg	623
Val Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val	
195 200 205	
caa cgc atg caa cct cca ggg atc cca cac tat ggt ctt gct tct cag	671
Gln Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln	
210 215 220	
gca gga atg ggt gga gta aat cct ggt ggc atc cca att cag cgg gga	719
Ala Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly	
225 230 235	

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gtt cct gct cag gct cat caa cag cag cag atg aga agg aaa gac cct 767
Val Pro Ala Gln Ala His Gln Gln Gln Gln Met Arg Arg Lys Asp Pro
240                245                250                255

gga atg ggg atg act gga tat cct cca caa cag aaa tca agg cgc ttt 815
Gly Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe
                260                265                270

tgagagtccg ggtggatttg gagcctaagt gggaggacaa atacacattc caatcaaatt 875

agaggaaacc ttaaattaat cttccagtca gctgaaacga caccagtggg accaaatgat 935

ctgaccccat ttccaggatt gcatgtatatt attaggagga atacacgaat gaagattcga 995

gtctagtgcc aaattattct aacatacctt catcatttgt tcctactaca ttccgacggt 1055

atatgtttca actagtggaa gggttttctgc agtccaccca tgtggcacaa acatgattca 1115

tagcatgcc aagcaacactt tactggtgtg taccaaggca atttctctat ttccaagcca 1175

aaaaaaaaa aaaaaaaaaa                                     1193

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<210> 56
<211> 271
<212> PRT
<213> Avicennia marina

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<400> 56
Ala Pro Glu Leu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val Asp
 1                5                10                15

Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys Pro
                20                25                30

Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln Leu
                35                40                45

Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln Glu
 50                55                60

Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val Gln
 65                70                75                80

Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val Val
                85                90                95

His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met Leu
                100                105                110

Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu His
                115                120                125

Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val Pro
                130                135                140

Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val Asp
145                150                155                160

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Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln Pro  
 165 170 175  
 Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His Val  
 180 185 190  
 Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val Gln  
 195 200 205  
 Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln Ala  
 210 215 220  
 Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly Val  
 225 230 235 240  
 Pro Ala Gln Ala His Gln Gln Gln Gln Met Arg Arg Lys Asp Pro Gly  
 245 250 255  
 Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe  
 260 265 270

<210> 57  
 <211> 1195  
 <212> DNA  
 <213> Sueada japonica

<220>  
 <221> CDS  
 <222> (116)..(1195)

<400> 57  
 gcaaaagttaa gaggtaaaga acacaaacca actttctatt ttcagctcaa atcaaattca 60  
 atagtggcaa aacaatagag ggcaaattct cattgcccaa ttcaaatttg gtaaa atg 118  
 Met  
 1  
 gct caa aag cat ttg aaa gaa ctt ctc aaa gaa gat caa gaa ccc ttt 166  
 Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro Phe  
 5 10 15  
 cat tta aag gat tac att gca act aaa aaa tgt caa ctt ttg aag aag 214  
 His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys Lys  
 20 25 30  
 caa gaa tta gta gta ccc aaa tca aaa ctt caa ctc aaa aag cca aag 262  
 Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro Lys  
 35 40 45  
 cca aaa cca att tca aaa agc act tca gtt ttg tgc aaa aat gct tgc 310  
 Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala Cys  
 50 55 60 65  
 ttt tta tct tta caa gaa tcc cct gac ctc aga aaa tcc ccc aaa cta 358  
 Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys Leu  
 70 75 80

ttt gat ttt cca cct tcc cct gtt tct aac aaa agc cca aac aga gta	406
Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg Val	
85 90 95	
ttc ctc aat gtt cct gct aaa act gct gct ctt ctt ctt gaa gct gct	454
Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala Ala	
100 105 110	
att cga att caa acc cac aaa tct aaa ccc aaa acc cag att aaa aat	502
Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys Asn	
115 120 125	
tcg ggt ttt ggg cta ttc ggg tca atg tta aag cga tta aat ctt cga	550
Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu Arg	
130 135 140 145	
aat cgt acc caa aaa atc aag tca aaa aca gag gaa caa aac aga gga	598
Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg Gly	
150 155 160	
tgc tct gtt ttg agg agt gtt gaa gaa gaa aaa act acc acc att tct	646
Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile Ser	
165 170 175	
tct tct tca tct tca tct tct tca aca tca tcg tat tct tcg tgt tct	694
Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys Ser	
180 185 190	
tgc aat gag agg tta agt agt ttg gat ttg gag agt tct agc agt gga	742
Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser Gly	
195 200 205	
aga tca tta cat gat gaa gat gaa gat gaa gat gaa gat gaa ttt	790
Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Glu Asp Asp Glu Phe	
210 215 220 225	
gag ttt aca aat gtt tta aga gaa aat aat aat gat gat aaa aat gga	838
Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn Gly	
230 235 240	
ggg tat tat tca gga att tgc tta agt cct ttg agt cca ttt cgt ttt	886
Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg Phe	
245 250 255	
gct ctt cat aaa aac tct tct cct gaa cgt tgc tct cct gct aaa tcc	934
Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys Ser	
260 265 270	
cct gtt cgt tgc aaa ttt gag ggt aat gct aaa tat gaa caa gaa agc	982
Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu Ser	
275 280 285	
tta ata aag ttt gaa gac gaa gat gaa gaa gac aaa gag caa aat agc	1030
Leu Ile Lys Phe Glu Asp Glu Asp Glu Glu Asp Lys Glu Gln Asn Ser	
290 295 300 305	

cct gtt tcc gtg ctc gat cct cca ttc gag gat gat tac gat ggg cat 1078  
 Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly His  
                   310                  315                  320

gag gag gat agc tac gag gac atc gaa tgc agc tat gct ttt gta caa 1126  
 Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val Gln  
                   325                  330                  335

aga gca caa caa gag tta ttg cac aga ctt cac cgg ttc cag aag cta 1174  
 Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys Leu  
                   340                  345                  350

gcg gag ttg gac cca att gaa 1195  
 Ala Glu Leu Asp Pro Ile Glu  
                   355                  360

<210> 58

<211> 360

<212> PRT

<213> Sueada japonica

<400> 58

Met Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro  
   1                                  5                                  10                                  15

Phe His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys  
                   20                                  25                                  30

Lys Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro  
                   35                                  40                                  45

Lys Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala  
                   50                                  55                                  60

Cys Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys  
                   65                                  70                                  75                                  80

Leu Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg  
                   85                                  90                                  95

Val Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala  
                   100                                  105                                  110

Ala Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys  
                   115                                  120                                  125

Asn Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu  
                   130                                  135                                  140

Arg Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg  
                   145                                  150                                  155                                  160

Gly Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile  
                   165                                  170                                  175

Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys  
                   180                                  185                                  190

Ser Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser  
 195 200 205  
 Gly Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Glu Asp Asp Glu  
 210 215 220  
 Phe Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn  
 225 230 235 240  
 Gly Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg  
 245 250 255  
 Phe Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys  
 260 265 270  
 Ser Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu  
 275 280 285  
 Ser Leu Ile Lys Phe Glu Asp Glu Asp Glu Glu Asp Lys Glu Gln Asn  
 290 295 300  
 Ser Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly  
 305 310 315 320  
 His Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val  
 325 330 335  
 Gln Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys  
 340 345 350  
 Leu Ala Glu Leu Asp Pro Ile Glu  
 355 360

<210> 59  
 <211> 1301  
 <212> DNA  
 <213> Salsola komarovii

<220>  
 <221> CDS  
 <222> (3)..(815)

<400> 59  
 gt gag gtt gac gat agc gtt aat agt cta cag gca gat gtt gac aac 47  
 Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn  
 1 5 10 15  
 ctt tca att gag gaa cgc aga ttg gat gaa cag ata agg gaa atg caa 95  
 Leu Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln  
 20 25 30  
 gaa aga ttg agg gaa atg agt gaa gat gat atc aat cag aag tgg ctt 143  
 Glu Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu  
 35 40 45



ttt gta act gaa gaa gac ata aag ggt tta cct tgt ttt cag aat gaa	191
Phe Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu	
50 55 60	
acc tta att gca att aaa gct cca cat gga aca act ttg gag gtt cca	239
Thr Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro	
65 70 75	
gat cca gat gag gct gtc gat tat cct caa aga aga tac aag ata gtt	287
Asp Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val	
80 85 90 95	
ctt agg agc aca atg ggt cct att gat gta tat tta gtc agt caa ttt	335
Leu Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe	
100 105 110	
gaa gag aag ttt gag gag atc agt ggt gct gac ggt cca cta agt ata	383
Glu Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile	
115 120 125	
cca agt acc tca ggt gat gac aaa cac aca act gtt gca gct aag gaa	431
Pro Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu	
130 135 140	
gaa agc aat ggc aat gag att gaa ata gaa gga caa ggg acc cat aga	479
Glu Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg	
145 150 155	
atc tgc tca gat tcc aac gct cag caa gac ttt gtg agt gga att atg	527
Ile Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met	
160 165 170 175	
aag ata gtg cct gaa gtt gat agt gat gca gat tac tgg ttg cta tcg	575
Lys Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser	
180 185 190	
gat gct gat gtt agc att act gac atg tgg gga act gat tct gga gtt	623
Asp Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val	
195 200 205	
gaa tgg aat gaa tta ggg act ata cat gaa gac tat gcc gtg gct aat	671
Glu Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn	
210 215 220	
gtt ggc act tca cag cca caa agt cca cca aca agt gca aca gaa gtg	719
Val Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val	
225 230 235	
ctt cca gct aac atg aca agc agg aga ttg aca tgg agt ttt gag aga	767
Leu Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg	
240 245 250 255	
att gcc aar att cat tca aat ggt cac tat tgc ttg gaa gtg agg ctc	815
Ile Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu	
260 265 270	
taactttcta ttattcatcc tgggatttgg gtacgaaagt ctgccttgaa gatgctgtaa	875

catgttgtgt attacaactg tgtgaatcta gtaagttggg aggggtgagat tgttcctgat 935  
 cttattgcac agccgggttg gagagattga tcgctcaaca actgacaaaa ttggggcatg 995  
 ttaacggata gtatgcagtt gtaattttgt acatcacatt tgttgatttt agtcagtaca 1055  
 tcataactag ctcttcctat acttcttcaa ttgtcaactg gaatagattt ttagattaat 1115  
 tagatctctc tttgtatgga aatgtttcag ggtaacaagc cagaaattaa aatgggttta 1175  
 tgtgtaaaaa tatatactta aattgtttgt aggaagtttc tgatggggtg ttggatggct 1235  
 tttacaact acatcgtata aggaaattcg tatcacaaat tcacaatgaa aaaaaaaaaa 1295  
 aaaaaa 1301

<210> 60

<211> 271

<212> PRT

<213> Salsola komarovii

<400> 60

Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn Leu  
 1 5 10 15

Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln Glu  
 20 25 30

Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu Phe  
 35 40 45

Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu Thr  
 50 55 60

Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro Asp  
 65 70 75 80

Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val Leu  
 85 90 95

Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe Glu  
 100 105 110

Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile Pro  
 115 120 125

Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu Glu  
 130 135 140

Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg Ile  
 145 150 155 160

Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met Lys  
 165 170 175

Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser Asp  
 180 185 190

Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val Glu  
 195 200 205

Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn Val  
 210 215 220

Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val Leu  
 225 230 235 240

Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg Ile  
 245 250 255

Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu  
 260 265 270

<210> 61  
 <211> 1032  
 <212> DNA  
 <213> Salsola komarovii

<220>  
 <221> CDS  
 <222> (1)..(732)

<400> 61  
 cca caa cga aga ccc gac ccg gtc ccg aac ctt cac ggt cag ctt ttt 48  
 Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe  
 1 5 10 15

caa cac cga aat cca cac cac cgt gac ctc cac ccc tgc cgt agc ccg 96  
 Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro  
 20 25 30

gca atg ggt cca ctc cct ccg cag act cat ctg cgc tgg tat tcc ctc 144  
 Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu  
 35 40 45

tcg cgc tac tcc ccc gtg atc ggc ctc ggc gtc caa tgg aag ccc tcc 192  
 Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser  
 50 55 60

tcc acc tca gct gcc act ctt caa ctc agc atc gac aaa aag tgc ctc 240  
 Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu  
 65 70 75 80

atc ttc caa ctc tcc cac tcc ccc gcc atc ccc gcc acc ctc cgc gac 288  
 Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp  
 85 90 95

ctc ctc ctc gac gat cgc gtc acc ttc ttt ggt gtc cac aac ggc cgt 336  
 Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg  
 100 105 110

gcc cgc gac ctc ctc caa ggg tcc cac cat gag ctc gac gtc aac aat 384  
 Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Val Asn Asn  
 115 120 125

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ctg gtt gat ctt gcc gag gag gaa aat ggt cat tac ttg aag tgg tcc 432
Leu Val Asp Leu Ala Glu Glu Asn Gly His Tyr Leu Lys Trp Ser
130 135 140

atg gaa gac atg gct gaa gat gtg ttg ggc ttt tgt ggg gta cac aaa 480
Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys
145 150 155 160

ccc agg aag gtt atg tta agt ggt tgg gat cag tat tgc ttg tct aat 528
Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn
165 170 175

gac cag gtt cag tat gct tgt gtt gat gct tac gtt tct ctt cgt ctt 576
Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu
180 185 190

gct cga gct tat ggg tac cac cgt ctc gat cac gat gat gat tat gat 624
Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp
195 200 205

gac cat gac gac gat gat aac gac cac acc gat gat gat tac gat gac 672
Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp
210 215 220

gtt tac gac cgc aat ata ggc tct gat gat gat ggt tat gat gcc gat 720
Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Gly Tyr Asp Ala Asp
225 230 235 240

gat gat cga cga tgatcaattt ggactagact tcgttattgg aagggtccga 772
Asp Asp Arg Arg

tcatcatgcc agtctaatta caaagagaca agaaataaaa atgatgatca aaaaaagaag 832

tcaatccata tacgtaattt tcattgcaat atcaattttg aggtgtttta ttattggcct 892

gtaataatag ttttatttaa taatagcact atagatctca tcctaacctt tacttattgg 952

gcttatgcgc tgtatgtcca ataaccaagt ttaatttatt tcatgatctg atgattactg 1012

caaaaaaaaa aaaaaaaaaa 1032

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<210> 62
<211> 244
<212> PRT
<213> Salsola komarovii

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<400> 62
Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe
1 5 10 15

Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro
20 25 30

Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu
35 40 45

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Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser  
 50 55 60  
 Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu  
 65 70 75 80  
 Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp  
 85 90 95  
 Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg  
 100 105 110  
 Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn  
 115 120 125  
 Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser  
 130 135 140  
 Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys  
 145 150 155 160  
 Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn  
 165 170 175  
 Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu  
 180 185 190  
 Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp  
 195 200 205  
 Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp  
 210 215 220  
 Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp  
 225 230 235 240  
 Asp Asp Arg Arg

<210> 63

<211> 1029

<212> DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (3)..(824)

<400> 63

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 gac acc cat ctt agt ctt aag cct ctc atg gcc acc gcg gta ttc tca 95  
 Asp Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser  
 20 25 30

cct tct gcc ctt cta tcc acc tcc aca tcc acc tca aca acc cct ctt	143
Pro Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Ser Thr Pro Leu	
35 40 45	
aaa gct ccc ccc ttg gcc tta acc aag acc cac gta acg atc cca tca	191
Lys Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser	
50 55 60	
tca tca aag cca ccc cta acc aat tta act acc agt tta act gct gtc	239
Ser Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val	
65 70 75	
gcc aca gct gct gcc ata atc ctg tcc aca acc cct cca tcg ttt gct	287
Ala Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala	
80 85 90 95	
gat gat ttg cag aca aat gca tac aac att tac tac ggc act gct gca	335
Asp Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala	
100 105 110	
agt gca gcc aat tat gga ggc tac ggt ggc aat tcg aac aag aaa gat	383
Ser Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp	
115 120 125	
tca gct gag tac ata tat gac gtc cct gca ggt tgg aaa gag aga cta	431
Ser Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu	
130 135 140	
gta tca aaa gtt gag aag ggt acc aat gga aca gat agt gag ttc ttc	479
Val Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe	
145 150 155	
aac ccc aag aag aag aca gag cga gag tac ctt acc tac ctt gct ggt	527
Asn Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly	
160 165 170 175	
att agg caa cta ggt ccc aaa gaa gtg atc ctc aac aac tta gca ctc	575
Ile Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu	
180 185 190	
tca gat gtg aac ctg caa gat caa att tcc agt gca gac tct gtg aca	623
Ser Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr	
195 200 205	
tca gaa gag agg aaa gat gac aag gga cag gtt tac tat gat tat gag	671
Ser Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu	
210 215 220	
att gct gga gct ggt tca cac agt ttg ata tcg gta aca tgt gcc agg	719
Ile Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg	
225 230 235	
aac aag cta tat gcg cat ttt gtt agc gca cca aca ccc gaa tgg aat	767
Asn Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn	
240 245 250 255	

cgg gat caa gat atg ctg agg cac atc cac aac tca ttt aca aca gtc 815  
 Arg Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val  
                   260                                  265                                  270

ggg tca ttc tagaaagtgt atatgataat catttataga gatgtcagag 864  
 Gly Ser Phe

aggcatacat ttgaatgtac ttctgatgag ctggacttct tgatctatgt aacattgtaa 924

cgaaaattct ttctgggtta tcagaaacct agtgagtgtc tgaaacttgc aatgagaaac 984

tcttcaataa acaatgactt gtatcaaaaa aaaaaaaaaa aaaaa 1029

<210> 64

<211> 274

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 64

His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu Asp  
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Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser Pro  
                   20                                  25                                  30

Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Ser Thr Thr Pro Leu Lys  
                   35                                  40                                  45

Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser Ser  
   50                                  55                                  60

Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val Ala  
   65                                  70                                  75                                  80

Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala Asp  
                   85                                  90                                  95

Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala Ser  
                   100                                  105                                  110

Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp Ser  
   115                                  120                                  125

Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu Val  
   130                                  135                                  140

Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe Asn  
   145                                  150                                  155                                  160

Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly Ile  
                   165                                  170                                  175

Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu Ser  
                   180                                  185                                  190

Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr Ser  
   195                                  200                                  205

Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu Ile  
 210 215 220

Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg Asn  
 225 230 235 240

Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn Arg  
 245 250 255

Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val Gly  
 260 265 270

Ser Phe

<210> 65

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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gctctgagaa ccgtctagac ttagatgaag gtg

33

<210> 66

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 66

tctctcggtc atctcgagct attacagctc

30